

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Hunter, Shirley Wu
Sim, Gek-Kee
Weber, Eric R.
- (ii) TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND
APPARATUS TO COLLECT SUCH PROTEINS
- (iii) NUMBER OF SEQUENCES: 88
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: SHERIDAN ROSS P.C.
(B) STREET: 1560 BROADWAY, SUITE 1200
(C) CITY: DENVER
(D) STATE: CO
(E) COUNTRY: U.S.A.
(F) ZIP: 80202
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/171,156
(B) FILING DATE: 1998-10-09
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Connell, Gary J.
(B) REGISTRATION NUMBER: 32,020
(C) REFERENCE/DOCKET NUMBER: 2618-17-C4-PUS
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 303/863-9700
(B) TELEFAX: 303/863-0223

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Gly | Asn | His | Val | Phe | Leu | Glu | Asp | Gly | Met | Ala | Asp | Met | Thr |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Gly | Gly | Gln | Gln | Met | Gly | Arg | Asp | Leu | Tyr | | | | | | |
| | | | | 20 | | | | 25 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:

10071751.000702

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Xaa = Tyr or Asp
- (B) LOCATION: 5

(ix) FEATURE:

- (A) NAME/KEY: Xaa = any amino acid
- (B) LOCATION: 6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Lys Tyr Arg Asn Xaa Xaa Thr Asn Asp Pro Gln Tyr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Glu Ile Lys Arg Asn Asp Arg Glu Pro Gly Asn Leu Ser Lys Ile Arg
 1 5 10 15

Thr Val Met Asp Lys Val Ile Lys Gln Thr Gln
 20 25

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Xaa = Ala or His
- (B) LOCATION: 8

(ix) FEATURE:

- (A) NAME/KEY: Xaa = Ala or His
- (B) LOCATION: 9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Lys Asp Asn Asp Ile Tyr Xaa Xaa Arg Asp Ile Asn Glu Ile Leu
 1 5 10 15

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

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(ix) FEATURE:
      (A) NAME/KEY: Xaa = any amino acid
      (B) LOCATION: 12
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

INFORMATION FOR SEQ ID NO:6:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

(2) INFORMATION FOR SEQ ID NO:7:

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
 (A) NAME/KEY: Xaa = any amino acid
 (B) LOCATION: 13

(ix) FEATURE:
 (A) NAME/KEY: Xaa = any amino acid
 (B) LOCATION: 19

(ix) FEATURE:
 (A) NAME/KEY: Xaa = any amino acid
 (B) LOCATION: 21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Tyr	Phe	Asn	Asp	Gln	Ile	Lys	Ser	Val	Met	Glu	Pro	Xaa	Val	Phe	Lys
1				5					10					15	
Tyr	Pro	Xaa	Ala	Xaa	Leu										
						20									

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..20
 (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGRTTTCWA TRAARTCTTC	20
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(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCGGCA CGAGTGAAAT TCAATATTTT GTTTTACATT AAATTTTTC AATTCGATAT	60
GAAATTTTCTA CTGGCAATTT GCGTGTGTG TGTTTATTA AATCAAGTAT CTATGTCAAA	120
AATGGTCACT GAAAAGTGTA AGTCAGGTGG AAATAATCCA AGTACAGAAG AGGTGTCAAT	180
ACCATCTGGG AAGCTTACTA TTGAAGATTT TTGTATTGGA AATCA	225

(2) INFORMATION FOR SEQ ID NO:10:

20071231-020702

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..15
 - (D) OTHER INFORMATION: /label= primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AATTCGGCAC GAGTG

15

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 565 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 45..314
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGAAATTCAA TATTTTGT	TTT TACATTAAAT TTTTCAAATT CGAT ATG AAA TTT TTA	56
	Met Lys Phe Leu	
	1	
CTG GCA ATT TGC GTG TTG TGT GTT TTA TTA AAT CAA GTA TCT ATG TCA	104	
Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln Val Ser Met Ser		
5 10 15 20		
AAA ATG GTC ACT GAA AAG TGT AAG TCA GGT GGA AAT AAT CCA AGT ACA	152	
Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser Thr		
25 30 35		
GAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT GAA GAT TTT TGT	200	
Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe Cys		
40 45 50		
ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TAC AAA AGT CAA TGT GGA	248	
Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys Ser Gln Cys Gly		
55 60 65		
TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA CGA CCA AAT CAA	296	
Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr Arg Pro Asn Gln		
70 75 80		
AAA CAC TGT TAT TGC GAA TAACCATATT CCGGATGAAA GACCAAATTG	344	
Lys His Cys Tyr Cys Glu		
85 90		

ATATAAATTA CTAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC 404
 CTAACATGTT TTGCCTCCAA TTTATTTTAA CAGCAAATTG CTGGAACCTA CCGTACCGTA 464
 ACTAAATGTT CAAGAAATAC TGAATGTTTA CAAATAGATT ATTATAAATA TTGTAACATT 524
 GTCTAATATT TATAAGAATT ATATAAATCT AATTGCAAAA A 565

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln 15
 1 5 10
 Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn 30
 20 25 30
 Asn Pro Ser Thr Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile 45
 35 40 45
 Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys 60
 50 55 60
 Ser Gln Cys Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr 80
 65 70 75 80
 Arg Pro Asn Gln Lys His Cys Tyr Cys Glu 90
 85 90

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 270 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG AAA TTT TTA CTG GCA ATT TGC GTG TTG TGT GTT TTA TTA AAT CAA 48
 Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln
 1 5 10 15
 GTA TCT ATG TCA AAA ATG GTC ACT GAA AAG TGT AAG TCA GGT GGA AAT 96
 Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn
 20 25 30

AAT CCA AGT ACA GAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT 144
 Asn Pro Ser Thr Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile
 35 40 45
 GAA GAT TTT TGT ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TAC AAA 192
 Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys
 50 55 60
 AGT CAA TGT GGA TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA 240
 Ser Gln Cys Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr
 65 70 75 80
 CGA CCA AAT CAA AAA CAC TGT TAT TGC GAA 270
 Arg Pro Asn Gln Lys His Cys Tyr Cys Glu
 85 90

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln
 1 5 10 15
 Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn
 20 25 30
 Asn Pro Ser Thr Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile
 35 40 45
 Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys
 50 55 60
 Ser Gln Cys Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr
 65 70 75 80
 Arg Pro Asn Gln Lys His Cys Tyr Cys Glu
 85 90

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGTGGATCCG TCAAAAATGG TCACTG

26

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /label= primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCGGAATTCG GTTATTCGCA ATAACAGT

28

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 897 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 97..567
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCGAAATCTC CTATCACAGT GTACGGAGTG TAAAATATTG TTGAAGTATT TTGAAATTTA 60

TTAATTTATT CGAAAAGGAG ATTTCAATTAA ATAAAA ATG GTT TAC GAA AGT GAC 114
Met Val Tyr Glu Ser Asp
1 5

TTT TAC ACG ACC CGT CGG CCC TAC AGT CGT CCG GCT TTG TCT TCA TAC 162
Phe Tyr Thr Thr Arg Arg Pro Tyr Ser Arg Pro Ala Leu Ser Ser Tyr
10 15 20

TCC GTA ACG GCA CGT CCA GAG CCG GTT CCT TGG GAC AAA TTG CCG TTC 210
Ser Val Thr Ala Arg Pro Glu Pro Val Pro Trp Asp Lys Leu Pro Phe
25 30 35

GTC CCC CGT CCA AGT TTG GTA GCA GAT CCC ATA ACA GCA TTT TGC AAG 258
Val Pro Arg Pro Ser Leu Val Ala Asp Pro Ile Thr Ala Phe Cys Lys
40 45 50

CGA AAA CCT CGC CGA GAA GAA GTT GTT CAA AAA GAG TCC ATT GTT CGA 306
Arg Lys Pro Arg Arg Glu Glu Val Val Gln Lys Glu Ser Ile Val Arg
55 60 65 70

AGG ATC AAT TCT GCA GGA ATT AAA CCC AGC CAG AGA GTT TTA TCG GCT 354
 Arg Ile Asn Ser Ala Gly Ile Lys Pro Ser Gln Arg Val Leu Ser Ala
 75 80 85

CCA ATA AGA GAA TAC GAA TCC CCA AGG GAC CAG ACC AGG CGT AAA GTT 402
 Pro Ile Arg Glu Tyr Glu Ser Pro Arg Asp Gln Thr Arg Arg Lys Val
 90 95 100

TTG GAA AGC GTC AGA AGA CAA GAA GCT TTT CTG AAC CAA GGA GGA ATT 450
 Leu Glu Ser Val Arg Arg Gln Glu Ala Phe Leu Asn Gln Gly Gly Ile
 105 110 115

TGT CCA TTG ACC ACC AGA AAT GAT GAC ATG GAT AGA CTT CTA CCC CGT 498
 Cys Pro Leu Thr Thr Arg Asn Asp Asp Met Asp Arg Leu Leu Pro Arg
 120 125 130

CTC CAC AGT TCA CAC ACA ACA CCT TCT GCG GAT AGG AAA GTT TTG TTG 546
 Leu His Ser Ser His Thr Pro Ser Ala Asp Arg Lys Val Leu Leu
 135 140 145 150

ACC ACT TTT CAC AGA AGA TAC T GATTAAAAAT GAAAGTTAAG AAATTTGTTG 598
 Thr Thr Phe His Arg Arg Tyr
 155

AAGTCATGTG GTGTTTTTTA TACATTCTTT ATTAATCGAT ATTCCTAACG AACGATACGA 658

TAACTTTCGA TAACTTTTTT TGGTTAATTT TGACAAAATA TGCATTTGCA AGCATAACAT 718

TCATTTTCAA GGCAAACGCT TTCTGATGAT TATCTTGTTA AAAGTGTGGA AACAAGCGTA 778

GTGTTAACAA ATGCATTGCT TGTGTTTGATT ATTTATTTAT CTATTATATA TTCCATATTG 838

TATTGTAGGT GGTGTAAGTT GTATTACTAA TACACGTACT TTGTGAAAAA AAAAAAAAAA 897

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Val Tyr Glu Ser Asp Phe Tyr Thr Thr Arg Arg Pro Tyr Ser Arg
 1 5 10 15

Pro Ala Leu Ser Ser Tyr Ser Val Thr Ala Arg Pro Glu Pro Val Pro
 20 25 30

Trp Asp Lys Leu Pro Phe Val Pro Arg Pro Ser Leu Val Ala Asp Pro
 35 40 45

Ile Thr Ala Phe Cys Lys Arg Lys Pro Arg Arg Glu Glu Val Val Gln
 50 55 60

Lys Glu Ser Ile Val Arg Arg Ile Asn Ser Ala Gly Ile Lys Pro Ser
 65 70 75 80

Gln Arg Val Leu Ser Ala Pro Ile Arg Glu Tyr Glu Ser Pro Arg Asp

85

90

95

Gln Thr Arg Arg Lys Val Leu Glu Ser Val Arg Arg Gln Glu Ala Phe
 100 105 110

Leu Asn Gln Gly Gly Ile Cys Pro Leu Thr Thr Arg Asn Asp Asp Met
 115 120 125

Asp Arg Leu Leu Pro Arg Leu His Ser Ser His Thr Thr Pro Ser Ala
 130 135 140

Asp Arg Lys Val Leu Leu Thr Thr Phe His Arg Arg Tyr
 145 150 155

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATGGTTTACG AAAGTGA CTTTACACGACC CGTCGGCCCT ACAGTCGTCC GGCTTTGTCT 60
 TCATACTCCG TAACGGCAGC TCCAGAGCCG GTTCCTTGGG ACAAATTGCC GTTCGTCCCC 120
 CGTCCAAGTT TGGTAGCAGA TCCCATAACA GCATTTTGCA AGCGAAAACC TCGCCGAGAA 180
 GAAGTTGTTC AAAAAGAGTC CATTGTTTGA AGGATCAATT CTGCAGGAAT TAAACCCAGC 240
 CAGAGAGTTT TATCGGCTCC AATAAGAGAA TACGAATCCC CAAGGGACCA GACCAGGCGT 300
 AAAGTTTGG AAAGCGTCAG AAGACAAGAA GCTTTTCTGA ACCAAGGAGG AATTTGTCCA 360
 TTGACCACCA GAAATGATGA CATGGATAGA CTTCTACCCC GTCTCCACAG TTCACACACA 420
 ACACCTTCTG CGGATAGGAA AGTTTTGTTG ACCACTTTTC ACAGAAGATA C 471

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2706 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 5..2706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCGG ATG AAG AGC ATC GAG GCT TAT ACA AAC AGA TAT GAA ATC ATA GCT 49
 Met Lys Ser Ile Glu Ala Tyr Thr Asn Arg Tyr Glu Ile Ile Ala
 1 5 10 15

TCT GAA ATA GTT AAT CTT CGA ATG AAA CCA GAT GAT TTT AAT TTA ATA Ser Glu Ile Val Asn Leu Arg Met Lys Pro Asp Asp Phe Asn Leu Ile 20 25 30	97
AAA GTT ATT GGT CGA GGA GCA TTT GGT GAA GTA CAG TTA GTG CGA CAC Lys Val Ile Gly Arg Gly Ala Phe Gly Glu Val Gln Leu Val Arg His 35 40 45	145
AAA TCA ACT GCA CAA GTT TTT GCT ATG AAA CGC CTA TCA AAA TTT GAA Lys Ser Thr Ala Gln Val Phe Ala Met Lys Arg Leu Ser Lys Phe Glu 50 55 60	193
ATG ATT AAG AGA CCA GAC TCT GCA TTT TTT TGG GAA GAA CGT CAT ATA Met Ile Lys Arg Pro Asp Ser Ala Phe Phe Trp Glu Glu Arg His Ile 65 70 75	241
ATG GCT CAT GCA AAA TCA GAA TGG ATT GTA CAA TTA CAT TTT GCT TTT Met Ala His Ala Lys Ser Glu Trp Ile Val Gln Leu His Phe Ala Phe 80 85 90 95	289
CAA GAT CAA AAA TAT CTT TAT ATG GTC ATG GAT TAT ATG CCG GGG GGT Gln Asp Gln Lys Tyr Leu Tyr Met Val Met Asp Tyr Met Pro Gly Gly 100 105 110	337
GAC TTG GTG AGT CTT ATG TCC GAT TAT GAA ATT CCA GAA AAA TGG GCA Asp Leu Val Ser Leu Met Ser Asp Tyr Glu Ile Pro Glu Lys Trp Ala 115 120 125	385
ATG TTC TAT ACA ATG GAA GTG GTG CTA GCA CTT GAT ACA ATT CAC TCC Met Phe Tyr Thr Met Glu Val Val Leu Ala Leu Asp Thr Ile His Ser 130 135 140	433
ATG GGA TTT GTA CAT CGT GAT GTT AAA CCT GAT AAT ATG CTT CTA GAC Met Gly Phe Val His Arg Asp Val Lys Pro Asp Asn Met Leu Leu Asp 145 150 155	481
AAA TAT GGT CAT TTA AAG TTA GCT GAC TTT GGA ACC TGT ATG AAA ATG Lys Tyr Gly His Leu Lys Leu Ala Asp Phe Gly Thr Cys Met Lys Met 160 165 170 175	529
GAT ACA GAT GGT TTG GTA CGT TCT AAT AAT GCT GTT GGA ACG CCT GAT Asp Thr Asp Gly Leu Val Arg Ser Asn Asn Ala Val Gly Thr Pro Asp 180 185 190	577
TAC ATT TCT CCC GAA GTT TTG CAG TCC CAA GGT GGT GAA GGA GTT TAC Tyr Ile Ser Pro Glu Val Leu Gln Ser Gln Gly Gly Glu Gly Val Tyr 195 200 205	625
GGT CGT GAA TGC GAT TGG TGG TCT GTG GGA ATT TTT TTG TAT GAA ATG Gly Arg Glu Cys Asp Trp Trp Ser Val Gly Ile Phe Leu Tyr Glu Met 210 215 220	673
TTA TTT GGA GAA ACA CCT TTT TAT GCA GAC AGT TTG GTT GGA ACT TAC Leu Phe Gly Glu Thr Pro Phe Tyr Ala Asp Ser Leu Val Gly Thr Tyr 225 230 235	721
AGT AAA ATT ATG GAT CAC AGA AAC TCA TTA ACT TTT CCT CCA GAA GTG Ser Lys Ile Met Asp His Arg Asn Ser Leu Thr Phe Pro Pro Glu Val 240 245 250 255	769

GAA ATA AGC CAA TAT GCC CGA TCT TTG ATA CAA GGA TTT TTA ACA GAC Glu Ile Ser Gln Tyr Ala Arg Ser Leu Ile Gln Gly Phe Leu Thr Asp 260 265 270	817
AGA ACA CAG CGT TTA GGC AGA AAT GAA GTG GAA GAA ATT AAA CGA CAT Arg Thr Gln Arg Leu Gly Arg Asn Glu Val Glu Glu Ile Lys Arg His 275 280 285	865
CCA TTT TTC ATA AAT GAT CAA TGG ACT TTT GAC AAT TTA AGA GAC TCT Pro Phe Phe Ile Asn Asp Gln Trp Thr Phe Asp Asn Leu Arg Asp Ser 290 295 300	913
GCC CCA CCT GTA GTG CCA GAG CTG AGT GGT GAT GAT GAT ACA AGG AAC Ala Pro Pro Val Val Pro Glu Leu Ser Gly Asp Asp Asp Thr Arg Asn 305 310 315	961
TTT GAT GAT ATT GAA CGT GAT GAA ACA CCT GAA GAG AAT TTT CCT ATA Phe Asp Asp Ile Glu Arg Asp Glu Thr Pro Glu Glu Asn Phe Pro Ile 320 325 330 335	1009
CCA AAA ACT TTT GCT GGT AAT CAT CTG CCA TTT GTT GGA TTC ACA TAT Pro Lys Thr Phe Ala Gly Asn His Leu Pro Phe Val Gly Phe Thr Tyr 340 345 350	1057
AAT GGT GAT TAC CAA TTA TTA ACA AAT GGA GGT GTT AGA AAT AGT GAT Asn Gly Asp Tyr Gln Leu Leu Thr Asn Gly Gly Val Arg Asn Ser Asp 355 360 365	1105
ATG GTT GAT ACA AAA TTA AAC AAC ATT TGT GTT TCA AGT AAG GAT GAT Met Val Asp Thr Lys Leu Asn Asn Ile Cys Val Ser Ser Lys Asp Asp 370 375 380	1153
GTG TTA AAT TTA CAA AAT TTA TTA GAA CAA GAG AAA GGT AAC AGT GAA Val Leu Asn Leu Gln Asn Leu Leu Glu Gln Glu Lys Gly Asn Ser Glu 385 390 395	1201
AAT TTG AAA ACA AAC ACC CAA TTA TTA AGT AAT AAA TTA GAT GAA CTA Asn Leu Lys Thr Asn Thr Gln Leu Leu Ser Asn Lys Leu Asp Glu Leu 400 405 410 415	1249
GGT CAG AGA GAA TGT GAA TTA AGG AAT CAG GCT GGA GAT TAT GAG AAA Gly Gln Arg Glu Cys Glu Leu Arg Asn Gln Ala Gly Asp Tyr Glu Lys 420 425 430	1297
GAA TTG ACT AAA TTC AAA TTA TCG TGC AAA GAA TTA CAA CGT AAG GCA Glu Leu Thr Lys Phe Lys Leu Ser Cys Lys Glu Leu Gln Arg Lys Ala 435 440 445	1345
GAA TTT GAG AAT GAA TTA CGG CGT AAA ACT GAG TCC TTA CTA GTT GAA Glu Phe Glu Asn Glu Leu Arg Arg Lys Thr Glu Ser Leu Leu Val Glu 450 455 460	1393
ACA AAG AAA AGA CTA GAC GAA GAG CAG AAT AAA AGA ACT AGA GAA ATG Thr Lys Lys Arg Leu Asp Glu Glu Gln Asn Lys Arg Thr Arg Glu Met 465 470 475	1441
AAT AAT AAT CAA CAG CAC AAT GAC AAA ATA AAT ATG TTA GAA AAA CAA Asn Asn Asn Gln Gln His Asn Asp Lys Ile Asn Met Leu Glu Lys Gln 480 485 490 495	1489
ATT AAT GAT TTA CAA GAA AAA TTG AAA GGT GAA TTA GAG CAC AAT CAG	1537

Ile Asn Asp Leu Gln Glu Lys Leu Lys Gly Glu Leu Glu His Asn Gln	
500 505 510	
AAA TTA AAG AAG CAA GCT GTT GAG CTT AGA GTT GCT CAG TCT GCT ACT	1585
Lys Leu Lys Lys Gln Ala Val Glu Leu Arg Val Ala Gln Ser Ala Thr	
515 520 525	
GAA CAA CTG AAT AAT GAA TTA CAG GAA ACT ATG CAG GGT TTA CAA ACA	1633
Glu Gln Leu Asn Asn Glu Leu Gln Glu Thr Met Gln Gly Leu Gln Thr	
530 535 540	
CAA AGA GAT GCT TTA CAA CAA GAA GTA GCA TCT CTC CAA GGC AAA CTT	1681
Gln Arg Asp Ala Leu Gln Gln Glu Val Ala Ser Leu Gln Gly Lys Leu	
545 550 555	
TCT CAA GAG AGG AGC TCT AGA TCA CAG GCT TCT GAT ATG CAG ATA GAA	1729
Ser Gln Glu Arg Ser Ser Arg Ser Gln Ala Ser Asp Met Gln Ile Glu	
560 565 570 575	
CTA GAA GCA AAA TTG CAG GCT CTC CAT ATT GAA CTG GAG CAT GTC AGA	1777
Leu Glu Ala Lys Leu Gln Ala Leu His Ile Glu Leu Glu His Val Arg	
580 585 590	
AAT TGT GAA GAC AAA GTT ACC CAA GAC AAC AGA CAA CTA TTG GAA AGG	1825
Asn Cys Glu Asp Lys Val Thr Gln Asp Asn Arg Gln Leu Leu Glu Arg	
595 600 605	
ATA TCA ACA TTG GAG AAA GAA TGT GCT TCT CTA GAA TTA GAA TTG AAA	1873
Ile Ser Thr Leu Glu Lys Glu Cys Ala Ser Leu Glu Leu Glu Leu Lys	
610 615 620	
GCA ACA CAA AAC AAA TAT GAG CAA GAG GTC AAA GCA CAT CGC GAA ACT	1921
Ala Thr Gln Asn Lys Tyr Glu Gln Glu Val Lys Ala His Arg Glu Thr	
625 630 635	
GAA AAA TCA AGA CTG GTC AGT AAA GAA GAA GCA AAT ATG GAG GAA GTT	1969
Glu Lys Ser Arg Leu Val Ser Lys Glu Glu Ala Asn Met Glu Glu Val	
640 645 650 655	
AAA GCA CTC CAA ATA AAA TTA AAT GAA GAG AAA TCT GCT CGA CAG AAA	2017
Lys Ala Leu Gln Ile Lys Leu Asn Glu Glu Lys Ser Ala Arg Gln Lys	
660 665 670	
TCT GAT CAG AAT TCT CAA GAA AAG GAA CGA CAA ATT TCT ATG TTA TCT	2065
Ser Asp Gln Asn Ser Gln Glu Lys Glu Arg Gln Ile Ser Met Leu Ser	
675 680 685	
GTG GAT TAT CGT CAA ATC CAA CAG CGT TTG CAA AAG CTA GAA GGA GAA	2113
Val Asp Tyr Arg Gln Ile Gln Gln Arg Leu Gln Lys Leu Glu Gly Glu	
690 695 700	
TAT AGG CAA GAG AGT GAA AAA GTT AAA GCT CTC CAC AGT CAG ATT GAG	2161
Tyr Arg Gln Glu Ser Glu Lys Val Lys Ala Leu His Ser Gln Ile Glu	
705 710 715	
CAA GAG CAA CTA AAA AAA TCA CAA TTA CAA AGC GAA TTG GGT GTT CAA	2209
Gln Glu Gln Leu Lys Lys Ser Gln Leu Gln Ser Glu Leu Gly Val Gln	
720 725 730 735	
AGG TCT CAG ACT GCA CAT TTA ACA GCC AGG GAA GCT CAG CTA GTT GGA	2257
Arg Ser Gln Thr Ala His Leu Thr Ala Arg Glu Ala Gln Leu Val Gly	

740

745

750

GAA GTT GCT CAT CTT AGA GAT GCT AAA AGA AAT GTT GAA GAA GAG TTA 2305
 Glu Val Ala His Leu Arg Asp Ala Lys Arg Asn Val Glu Glu Glu Leu
 755 760 765

CAC AAG TTA AAA ACT GCT CGA TCA GTG GAT AAT GCT CAG ATG AAA GAG 2353
 His Lys Leu Lys Thr Ala Arg Ser Val Asp Asn Ala Gln Met Lys Glu
 770 775 780

CTT CAA GAA CAA GTT GAA GCC GAG CAA GTT TTC TCG ACT CTT TAT AAA 2401
 Leu Gln Glu Gln Val Glu Ala Glu Gln Val Phe Ser Thr Leu Tyr Lys
 785 790 795

ACA CAT TCT AAT GAA CTT AAG GAA GAA CTT GAG GAA AAA TCT CGT CAT 2449
 Thr His Ser Asn Glu Leu Lys Glu Glu Leu Glu Glu Lys Ser Arg His
 800 805 810 815

ATT CAA GAA ATG GAA GAA GAA AGA GAA AGT TTG GTT CAT CAG CTA CAA 2497
 Ile Gln Glu Met Glu Glu Glu Arg Glu Ser Leu Val His Gln Leu Gln
 820 825 830

ATT GCA TTA GCT AGA GCT GAT TCA GAG GCA TTG GCG AGA TCA ATA GCT 2545
 Ile Ala Leu Ala Arg Ala Asp Ser Glu Ala Leu Ala Arg Ser Ile Ala
 835 840 845

GAT GAA AGT ATA GCT GAT TTA GAA AAG GAA AAG ACT ATG AAG GAA TTA 2593
 Asp Glu Ser Ile Ala Asp Leu Glu Lys Glu Lys Thr Met Lys Glu Leu
 850 855 860

GAA CTA AAA GAA TTA TTA AAC AAA AAT CGT ACT GAA CTT TCC CAG AAA 2641
 Glu Leu Lys Glu Leu Leu Asn Lys Asn Arg Thr Glu Leu Ser Gln Lys
 865 870 875

GAC ATT TCA ATA AGT GCA TTG CGT GAA CGA GAA AAT GAA CAG AAG AAA 2689
 Asp Ile Ser Ile Ser Ala Leu Arg Glu Arg Glu Asn Glu Gln Lys Lys
 880 885 890 895

CTT TTA GAA CAA ATC TC 2706
 Leu Leu Glu Gln Ile
 900

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Lys Ser Ile Glu Ala Tyr Thr Asn Arg Tyr Glu Ile Ile Ala Ser
 1 5 10 15
 Glu Ile Val Asn Leu Arg Met Lys Pro Asp Asp Phe Asn Leu Ile Lys
 20 25 30
 Val Ile Gly Arg Gly Ala Phe Gly Glu Val Gln Leu Val Arg His Lys
 35 40 45

Ser Thr Ala Gln Val Phe Ala Met Lys Arg Leu Ser Lys Phe Glu Met
 50 55 60
 Ile Lys Arg Pro Asp Ser Ala Phe Phe Trp Glu Glu Arg His Ile Met
 65 70 75 80
 Ala His Ala Lys Ser Glu Trp Ile Val Gln Leu His Phe Ala Phe Gln
 85 90 95
 Asp Gln Lys Tyr Leu Tyr Met Val Met Asp Tyr Met Pro Gly Gly Asp
 100 105 110
 Leu Val Ser Leu Met Ser Asp Tyr Glu Ile Pro Glu Lys Trp Ala Met
 115 120 125
 Phe Tyr Thr Met Glu Val Val Leu Ala Leu Asp Thr Ile His Ser Met
 130 135 140
 Gly Phe Val His Arg Asp Val Lys Pro Asp Asn Met Leu Leu Asp Lys
 145 150 155 160
 Tyr Gly His Leu Lys Leu Ala Asp Phe Gly Thr Cys Met Lys Met Asp
 165 170 175
 Thr Asp Gly Leu Val Arg Ser Asn Asn Ala Val Gly Thr Pro Asp Tyr
 180 185 190
 Ile Ser Pro Glu Val Leu Gln Ser Gln Gly Gly Glu Gly Val Tyr Gly
 195 200 205
 Arg Glu Cys Asp Trp Trp Ser Val Gly Ile Phe Leu Tyr Glu Met Leu
 210 215 220
 Phe Gly Glu Thr Pro Phe Tyr Ala Asp Ser Leu Val Gly Thr Tyr Ser
 225 230 235 240
 Lys Ile Met Asp His Arg Asn Ser Leu Thr Phe Pro Pro Glu Val Glu
 245 250 255
 Ile Ser Gln Tyr Ala Arg Ser Leu Ile Gln Gly Phe Leu Thr Asp Arg
 260 265 270
 Thr Gln Arg Leu Gly Arg Asn Glu Val Glu Glu Ile Lys Arg His Pro
 275 280 285
 Phe Phe Ile Asn Asp Gln Trp Thr Phe Asp Asn Leu Arg Asp Ser Ala
 290 295 300
 Pro Pro Val Val Pro Glu Leu Ser Gly Asp Asp Asp Thr Arg Asn Phe
 305 310 315 320
 Asp Asp Ile Glu Arg Asp Glu Thr Pro Glu Glu Asn Phe Pro Ile Pro
 325 330 335
 Lys Thr Phe Ala Gly Asn His Leu Pro Phe Val Gly Phe Thr Tyr Asn
 340 345 350
 Gly Asp Tyr Gln Leu Leu Thr Asn Gly Gly Val Arg Asn Ser Asp Met
 355 360 365

Val Asp Thr Lys Leu Asn Asn Ile Cys Val Ser Ser Lys Asp Asp Val
370 375 380

Leu Asn Leu Gln Asn Leu Leu Glu Gln Glu Lys Gly Asn Ser Glu Asn
385 390 395 400

Leu Lys Thr Asn Thr Gln Leu Leu Ser Asn Lys Leu Asp Glu Leu Gly
405 410 415

Gln Arg Glu Cys Glu Leu Arg Asn Gln Ala Gly Asp Tyr Glu Lys Glu
420 425 430

Leu Thr Lys Phe Lys Leu Ser Cys Lys Glu Leu Gln Arg Lys Ala Glu
435 440 445

Phe Glu Asn Glu Leu Arg Arg Lys Thr Glu Ser Leu Leu Val Glu Thr
450 455 460

Lys Lys Arg Leu Asp Glu Glu Gln Asn Lys Arg Thr Arg Glu Met Asn
465 470 475 480

Asn Asn Gln Gln His Asn Asp Lys Ile Asn Met Leu Glu Lys Gln Ile
485 490 495

Asn Asp Leu Gln Glu Lys Leu Lys Gly Glu Leu Glu His Asn Gln Lys
500 505 510

Leu Lys Lys Gln Ala Val Glu Leu Arg Val Ala Gln Ser Ala Thr Glu
515 520 525

Gln Leu Asn Asn Glu Leu Gln Glu Thr Met Gln Gly Leu Gln Thr Gln
530 535 540

Arg Asp Ala Leu Gln Gln Glu Val Ala Ser Leu Gln Gly Lys Leu Ser
545 550 555 560

Gln Glu Arg Ser Ser Arg Ser Gln Ala Ser Asp Met Gln Ile Glu Leu
565 570 575

Glu Ala Lys Leu Gln Ala Leu His Ile Glu Leu Glu His Val Arg Asn
580 585 590

Cys Glu Asp Lys Val Thr Gln Asp Asn Arg Gln Leu Leu Glu Arg Ile
595 600 605

Ser Thr Leu Glu Lys Glu Cys Ala Ser Leu Glu Leu Glu Lys Ala
610 615 620

Thr Gln Asn Lys Tyr Glu Gln Glu Val Lys Ala His Arg Glu Thr Glu
625 630 635 640

Lys Ser Arg Leu Val Ser Lys Glu Glu Ala Asn Met Glu Glu Val Lys
645 650 655

Ala Leu Gln Ile Lys Leu Asn Glu Glu Lys Ser Ala Arg Gln Lys Ser
660 665 670

Asp Gln Asn Ser Gln Glu Lys Glu Arg Gln Ile Ser Met Leu Ser Val
675 680 685

Asp Tyr Arg Gln Ile Gln Gln Arg Leu Gln Lys Leu Glu Gly Glu Tyr

AAC ATT ATT AGT ACT ACT GAT GAG AAT GGA AAT GTG ATT AGC ATT ACT 95
Asn Ile Ile Ser Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr
20 25 30
GAT GAG AAT GGA AAC ATT ATT AGT ACT ACT GAT GAG AAT GGA AAT GTG 143
Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp Glu Asn Gly Asn Val
35 40 45
ATT AGC ATT ACT GAT GAA AAT GGA AAC ATT ATT AGT ACT ACT GAT GAG 191
Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp Glu
50 55 60
AAT GGA AAT GTG ATT AGC ATT ACT GAT GAG AAT GGA AAT GTG ATT AGC 239
Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Val Ile Ser
65 70 75
ATT ACT GAT GAA AAT GGA AAC TCG AAT AGC ACT ACT AGT GTT TTC AAT 287
Ile Thr Asp Glu Asn Gly Asn Ser Asn Ser Thr Thr Ser Val Phe Asn
80 85 90 95
GAA ACT GAA AAT ATG ACT GGT GCT GCT GAT ACA AAT GAA TAT TCA ATT 335
Glu Thr Glu Asn Met Thr Gly Ala Ala Asp Thr Asn Glu Tyr Ser Ile
100 105 110
GGT TCT ACT GAC GGA AAT GGA AAT TTT ATA AGT ACT TTT AGT GAT CAT 383
Gly Ser Thr Asp Gly Asn Gly Asn Phe Ile Ser Thr Phe Ser Asp His
115 120 125
GAT TAC GTA AGT AAT ACT GAA GAA AAT GAA A 414
Asp Tyr Val Ser Asn Thr Glu Glu Asn Glu
130 135

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ala Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn
1 5 10 15
Ile Ile Ser Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp
20 25 30
Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp Glu Asn Gly Asn Val Ile
35 40 45
Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp Glu Asn
50 55 60
Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Val Ile Ser Ile
65 70 75 80
Thr Asp Glu Asn Gly Asn Ser Asn Ser Thr Thr Ser Val Phe Asn Glu
85 90 95

Thr Glu Asn Met Thr Gly Ala Ala Asp Thr Asn Glu Tyr Ser Ile Gly
100 105 110

Ser Thr Asp Gly Asn Gly Asn Phe Ile Ser Thr Phe Ser Asp His Asp
115 120 125

Tyr Val Ser Asn Thr Glu Glu Asn Glu
130 135

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 3..273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AT GAG AAT GGA AAT GTG ATT AGC TAT ACT GAT GAA AAT GGA AAC ATT	47
Glu Asn Gly Asn Val Ile Ser Tyr Thr Asp Glu Asn Gly Asn Ile	
1 5 10 15	
ATC AGT ACT ACT GAT GAG AAT GGA AAT GTG ATT AGC ATT ACT GAT GAA	95
Ile Ser Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu	
20 25 30	
AAT GGA AAT GTG ATT AGC ATT ACT GAT GAA AAT GGA AAC ATT ATC AGT	143
Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser	
35 40 45	
ACT ACT GAT GAG AAT GGA AAT GTG ATT AGC ATT ACT GAT GAA AAT GGA	191
Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly	
50 55 60	
AAT GTG ATT AGC ATT ACT GAT GAA AAT GGA AAC ATT ATT AGT ACT ACT	239
Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr	
65 70 75	
GAT GAG AAT GGA AAT GTG ATT AGC AAT ACT CGA G	273
Asp Glu Asn Gly Asn Val Ile Ser Asn Thr Arg	
80 85 90	

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Glu Asn Gly Asn Val Ile Ser Tyr Thr Asp Glu Asn Gly Asn Ile Ile
 1 5 10 15
 Ser Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn
 20 25 30
 Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr
 35 40 45
 Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn
 50 55 60
 Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp
 65 70 75 80
 Glu Asn Gly Asn Val Ile Ser Asn Thr Arg
 85 90

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1704 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 24..1406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CAGAAACCCG ACATTCTCAA AAT ATG GAA CCT CAA TCG CTG TCT TGG CAA	50
Met Glu Pro Gln Ser Leu Ser Trp Gln	
1 5	
CTT CCG ACT CAA GTA GTT CAG CCA GTT TTT GAA CAA CAA ATG CAG ATT	98
Leu Pro Thr Gln Val Val Gln Pro Val Phe Glu Gln Gln Met Gln Ile	
10 15 20 25	
CCT GGA TAT AAT ATG CAA ATT CAA TCT AAT TAT TAT CAA ATT CAC CCA	146
Pro Gly Tyr Asn Met Gln Ile Gln Ser Asn Tyr Tyr Gln Ile His Pro	
30 35 40	
GAA ATG TTG GAT CCA AAT TTG AAC AAT CCT CAG CAG TTA ATG TTT AAT	194
Glu Met Leu Asp Pro Asn Leu Asn Asn Pro Gln Gln Leu Met Phe Asn	
45 50 55	
TAT ATG CAA TTA CAA CAA TTG CAG GAA CTA CAA CAT TTA AGT CAA CAA	242
Tyr Met Gln Leu Gln Gln Leu Gln Glu Leu Gln His Leu Ser Gln Gln	
60 65 70	
CAG CCA ATG CAT CAT GAA TTT GAA CAT CAT ATC CCC ATT CCA CAA GAA	290
Gln Pro Met His His Glu Phe Glu His His Ile Pro Ile Pro Gln Glu	
75 80 85	
GCA ACT TCA ACT AAT TAC GGT CCA TCC GGA CAG TAT ATT ACT AGT GAC	338
Ala Thr Ser Thr Asn Tyr Gly Pro Ser Gly Gln Tyr Ile Thr Ser Asp	
90 95 100 105	

GCA ACA TCT TAT CAA TCA ATT GCC CAA CAA TTT GTA CCA CAA CCA CCA Ala Thr Ser Tyr Gln Ser Ile Ala Gln Gln Phe Val Pro Gln Pro Pro 110 115 120	386
ATT GAA ACT ACC ACC ACG AAA ATA CCT GAA ACT GAA ATT CAA ATT GGC Ile Glu Thr Thr Thr Thr Lys Ile Pro Glu Thr Glu Ile Gln Ile Gly 125 130 135	434
GTT TCG AAT CAA TAT GCC CAA AAT ATA ACT TAT AAT TCA AAT ATC AGT Val Ser Asn Gln Tyr Ala Gln Asn Ile Thr Tyr Asn Ser Asn Ile Ser 140 145 150	482
CCT GAA GTG ATT GGA TTC CGA GAA CAT TAT GTT GCG GAA CAG CCT TCT Pro Glu Val Ile Gly Phe Arg Glu His Tyr Val Ala Glu Gln Pro Ser 155 160 165	530
GGT GAC GTG CTT CAC AAA AGT CAT TTA ACA GAA CAA CCA GCA GAT AAA Gly Asp Val Leu His Lys Ser His Leu Thr Glu Gln Pro Ala Asp Lys 170 175 180 185	578
AGC ACA CGT GGT GAT CAG GAA CCT GTT AGT GAG ACA GGC TCT GGT TTT Ser Thr Arg Gly Asp Gln Glu Pro Val Ser Glu Thr Gly Ser Gly Phe 190 195 200	626
TCG TAT GCA CAA ATT TTA TCA CAG GGA CTT AAG CCT ACC CAG CCA TCC Ser Tyr Ala Gln Ile Leu Ser Gln Gly Leu Lys Pro Thr Gln Pro Ser 205 210 215	674
AAC TCA GTT AAT TTG CTT GCA GAT CGA TCG AGA TCA CCT CTA GAT ACG Asn Ser Val Asn Leu Leu Ala Asp Arg Ser Arg Ser Pro Leu Asp Thr 220 225 230	722
AAA ACG AAA GAA AAT TAT AAA TCT CCT GGT CGT GTG CAG GAT ATC ACG Lys Thr Lys Glu Asn Tyr Lys Ser Pro Gly Arg Val Gln Asp Ile Thr 235 240 245	770
AAA ATA ATA GAT GAG AAA CAA AAG TCG TCA AAA GAC ACA GAG TGG CAT Lys Ile Ile Asp Glu Lys Gln Lys Ser Ser Lys Asp Thr Glu Trp His 250 255 260 265	818
AAT AAG AAA GTG AAA GAA CAT AAA AAA GTG AAA GAT ATC AAA CCT GAT Asn Lys Lys Val Lys Glu His Lys Lys Val Lys Asp Ile Lys Pro Asp 270 275 280	866
TTC GAA TCT TCT CAA AGG AAT AAG AAA AGC AAG AAT ATT CCT AAG CAA Phe Glu Ser Ser Gln Arg Asn Lys Lys Ser Lys Asn Ile Pro Lys Gln 285 290 295	914
ATT GAA AAT ATC ACA CCT CAA CTT GAC AGC TTA CGA TCA CGA GAT ATA Ile Glu Asn Ile Thr Pro Gln Leu Asp Ser Leu Arg Ser Arg Asp Ile 300 305 310	962
GTA ATT AAG GGA GAA TTA CTA ACA AAA GAT ACT ACA AAA AGT TTA ACT Val Ile Lys Gly Glu Leu Leu Thr Lys Asp Thr Thr Lys Ser Leu Thr 315 320 325	1010
ACT GTT AAT GTT GAT AGT GAA TTA GAT AGT GTA AAA CCT AAA GAT GAA Thr Val Asn Val Asp Ser Glu Leu Asp Ser Val Lys Pro Lys Asp Glu 330 335 340 345	1058

AAA CCT GAA CCT TCT GAA CCT AGT AAA ACG TTT ATT GAT ACT TCA GTT 1106
Lys Pro Glu Pro Ser Glu Pro Ser Lys Thr Phe Ile Asp Thr Ser Val
350 355 360

GCA AAG GAT GTT GAT AAT TCT ACA CAG GCG AAC CAT AAA AAG AAG AAA 1154
Ala Lys Asp Val Asp Asn Ser Thr Gln Ala Asn His Lys Lys Lys Lys
365 370 375

AGT AAA TCT AAG CCG AGG AAA ACG GAA CCG GAA GAT GAA ATT GAA AAA 1202
Ser Lys Ser Lys Pro Arg Lys Thr Glu Pro Glu Asp Glu Ile Glu Lys
380 385 390

GCT TTG AAA GAA ATT CAA GCT AGT GAG AAA AAA CTT ACG AAG TCT ATC 1250
~~Ala~~ Leu Lys Glu Ile Gln Ala Ser Glu Lys Lys Leu Thr Lys Ser Ile
395 400 405

GAT AAC ATT GTG AAT AAA TTT AAT ACA CCA CTT GCT AGT GTT AAA GCC 1298
Asp Asn Ile Val Asn Lys Phe Asn Thr Pro Leu Ala Ser Val Lys Ala
410 415 420 425

GAT GAT TCC AAT TCT ACC AAG GAT AAT GTA CCA GCA AAG AAG AAA AAA 1346
Asp Asp Ser Asn Ser Thr Lys Asp Asn Val Pro Ala Lys Lys Lys Lys
430 435 440

CCT TCG AAG TCA TCT GTT TCT TTA CCT GAG AAT GTA GTA CAA AAT CTA 1394
Pro Ser Lys Ser Ser Val Ser Leu Pro Glu Asn Val Val Gln Asn Leu
445 450 455

TTG ATA CTA ACA TAA CTACTAGTAG CGACAAGATT GAAAACATGC CGCAACCGCA 1449
Leu Ile Leu Thr
460

ACCAAAAAGA GAAGATTTAC AAGATGCAGC TAAGGAAGTA TTGACTTCAA TAGAGTCAGT 1509

AATGATGCAG TCTGTTGAGA CTATTCCTAT TACGAAGAAA AGAGTAAATA AGAAAAAGAA 1569

TACCACTCAA CAGACGAAGG AATTTGTGGA ACACGAAATA TGCGATACAT CAAAAAATGA 1629

AACTTTAAAA AATATTGAAA AAGAATCGCA TGAGAATATG GCTATATTGC AAACAAGTCC 1689

GAAACCGCCA CTAAG 1704

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Glu Pro Gln Ser Leu Ser Trp Gln Leu Pro Thr Gln Val Val Gln
1 5 10 15

Pro Val Phe Glu Gln Gln Met Gln Ile Pro Gly Tyr Asn Met Gln Ile
20 25 30

Gln Ser Asn Tyr Tyr Gln Ile His Pro Glu Met Leu Asp Pro Asn Leu

10074351-020702

35	40	45
Asn Asn Pro Gln Gln Leu Met Phe Asn Tyr Met Gln Leu Gln Gln Leu		
50	55	60
Gln Glu Leu Gln His Leu Ser Gln Gln Gln Pro Met His His Glu Phe		
65	70	75 80
Glu His His Ile Pro Ile Pro Gln Glu Ala Thr Ser Thr Asn Tyr Gly		
	85	90 95
Pro Ser Gly Gln Tyr Ile Thr Ser Asp Ala Thr Ser Tyr Gln Ser Ile		
	100	105 110
Ala Gln Gln Phe Val Pro Gln Pro Pro Ile Glu Thr Thr Thr Thr Lys		
	115	120 125
Ile Pro Glu Thr Glu Ile Gln Ile Gly Val Ser Asn Gln Tyr Ala Gln		
	130	135 140
Asn Ile Thr Tyr Asn Ser Asn Ile Ser Pro Glu Val Ile Gly Phe Arg		
	145	150 155 160
Glu His Tyr Val Ala Glu Gln Pro Ser Gly Asp Val Leu His Lys Ser		
	165	170 175
His Leu Thr Glu Gln Pro Ala Asp Lys Ser Thr Arg Gly Asp Gln Glu		
	180	185 190
Pro Val Ser Glu Thr Gly Ser Gly Phe Ser Tyr Ala Gln Ile Leu Ser		
	195	200 205
Gln Gly Leu Lys Pro Thr Gln Pro Ser Asn Ser Val Asn Leu Leu Ala		
	210	215 220
Asp Arg Ser Arg Ser Pro Leu Asp Thr Lys Thr Lys Glu Asn Tyr Lys		
	225	230 235 240
Ser Pro Gly Arg Val Gln Asp Ile Thr Lys Ile Ile Asp Glu Lys Gln		
	245	250 255
Lys Ser Ser Lys Asp Thr Glu Trp His Asn Lys Lys Val Lys Glu His		
	260	265 270
Lys Lys Val Lys Asp Ile Lys Pro Asp Phe Glu Ser Ser Gln Arg Asn		
	275	280 285
Lys Lys Ser Lys Asn Ile Pro Lys Gln Ile Glu Asn Ile Thr Pro Gln		
	290	295 300
Leu Asp Ser Leu Arg Ser Arg Asp Ile Val Ile Lys Gly Glu Leu Leu		
	305	310 315 320
Thr Lys Asp Thr Thr Lys Ser Leu Thr Thr Val Asn Val Asp Ser Glu		
	325	330 335
Leu Asp Ser Val Lys Pro Lys Asp Glu Lys Pro Glu Pro Ser Glu Pro		
	340	345 350
Ser Lys Thr Phe Ile Asp Thr Ser Val Ala Lys Asp Val Asp Asn Ser		
	355	360 365

Thr Gln Ala Asn His Lys Lys Lys Lys Ser Lys Ser Lys Pro Arg Lys
 370 375 380

Thr Glu Pro Glu Asp Glu Ile Glu Lys Ala Leu Lys Glu Ile Gln Ala
 385 390 395 400

Ser Glu Lys Lys Leu Thr Lys Ser Ile Asp Asn Ile Val Asn Lys Phe
 405 410 415

Asn Thr Pro Leu Ala Ser Val Lys Ala Asp Asp Ser Asn Ser Thr Lys
 420 425 430

Asp Asn Val Pro Ala Lys Lys Lys Lys Pro Ser Lys Ser Ser Val Ser
 435 440 445

Leu Pro Glu Asn Val Val Gln Asn Leu Leu Ile Leu Thr
 450 455 460

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATGGAACCTC AATCGCTGTC TTGGCAACTT CCGACTCAAG TAGTTCAGCC AGTTTTTGAA 60

CAACAAATGC AGATTCCTGG ATATAATATG CAAATTCAAT CTAATTATTA TCAAATTCAC 120

CCAGAAATGT TGGATCCAAA TTTGAACAAT CCTCAGCAGT TAATGTTTAA TTATATGCAA 180

TTACAACAAT TGCAGGAACT ACAACATTTA AGTCAACAAC AGCCAATGCA TCATGAATTT 240

GAACATCATA TCCCCATTCC ACAAGAAGCA ACTTCAACTA ATTACGGTCC ATCCGGACAG 300

TATATTACTA GTGACGCAAC ATCTTATCAA TCAATTGCCC AACAATTTGT ACCACAACCA 360

CCAATTGAAA CTACCACCAC GAAAATACCT GAAACTGAAA TTCAAATTGG CGTTTCGAAT 420

CAATATGCCC AAAATATAAC TTATAATTCA AATATCAGTC CTGAAGTGAT TGGATTCCGA 480

GAACATTATG TTGCGGAACA GCCTTCTGGT GACGTGCTTC ACAAAAGTCA TTAAACAGAA 540

CAACCAGCAG ATAAAAGCAC ACGTGGTGAT CAGGAACCTG TTAGTGAGAC AGGCTCTGGT 600

TTTTTCGTATG CACAAATTTT ATCACAGGGA CTTAAGCCTA CCCAGCCATC CAACTCAGTT 660

AATTTGCTTG CAGATCGATC GAGATCACCT CTAGATACGA AAACGAAAGA AAATTATAAA 720

TCTCCTGGTC GTGTGCAGGA TATCACGAAA ATAATAGATG AGAAACAAAA GTCGTCAAAA 780

GACACAGAGT GGCATAATAA GAAAGTGAAA GAACATAAAA AAGTGAAAGA TATCAAACCT 840

GATTTTCGAAT CTTCTCAAAG GAATAAGAAA AGCAAGAATA TTCCTAAGCA AATTGAAAAAT 900

ATCACACCTC AACTTGACAG CTTACGATCA CGAGATATAG TAATTAAGGG AGAATTACTA 960
 ACAAAAAGATA CTACAAAAAG TTAACTACT GTTAATGTTG ATAGTGAATT AGATAGTGTA 1020
 AAACCTAAAG ATGAAAAACC TGAACCTTCT GAACCTAGTA AAACGTTTAT TGATACTTCA 1080
 GTTGCAAAGG ATGTTGATAA TTCTACACAG GCGAACCATA AAAAGAAGAA AAGTAAATCT 1140
 AAGCCGAGGA AAACGGAACC GGAAGATGAA ATTGAAAAAG CTTTGAAAGA AATTCAAGCT 1200
 AGTGAGAAAA AACTTACGAA GTCTATCGAT AACATTGTGA ATAAATTTAA TACACCACTT 1260
 GCTAGTGTTA AAGCCGATGA TTCCAATTCT ACCAAGGATA ATGTACCAGC AAAGAAGAAA 1320
 AAACCTTCGA AGTCATCTGT TTCTTTACCT GAGAATGTAG TACAAAATCT ATTGATACTA 1380
 ACA 1383

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1758 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1...1758

- (ix) FEATURE:
 (A) NAME/KEY: W = A or T
 (B) LOCATION: 1136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTA GAG ATG GCT AAA TTT CTG ACG GAA ACA TTA GAC GAC ATG ACT CTA 48
 Leu Glu Met Ala Lys Phe Leu Thr Glu Thr Leu Asp Asp Met Thr Leu
 1 5 10 15
 CAA CAC AAA GAT CAC AGA TCA GAA TTG GCT AAA GAG TTT TCA ATT TGG 96
 Gln His Lys Asp His Arg Ser Glu Leu Ala Lys Glu Phe Ser Ile Trp
 20 25 30
 TTT ACG AAA ATG AGA CAG TCT GGC GCT CAA GCC AGT AAC GAA GAA ATC 144
 Phe Thr Lys Met Arg Gln Ser Gly Ala Gln Ala Ser Asn Glu Glu Ile
 35 40 45
 ATG AAA TTT TCA AAA TTG TTT GAA GAT GAA ATC ACT CTT GAC TCG CTG 192
 Met Lys Phe Ser Lys Leu Phe Glu Asp Glu Ile Thr Leu Asp Ser Leu
 50 55 60
 GCG AGG CCG CAA CTT GTT GCT TTG TGC AGG GTA CTA GAA ATC AGT ACT 240
 Ala Arg Pro Gln Leu Val Ala Leu Cys Arg Val Leu Glu Ile Ser Thr
 65 70 75 80
 TTA GGA ACA ACA AAT TTC TTA AGG TTT CAA CTG CGA ATG AAA CTG CGT 288
 Leu Gly Thr Thr Asn Phe Leu Arg Phe Gln Leu Arg Met Lys Leu Arg
 85 90 95

TCA TTA GCT GCT GAT GAT AAA ATG ATT CAA AAA GAA GGC ATA GTT TCT	336
Ser Leu Ala Ala Asp Asp Lys Met Ile Gln Lys Glu Gly Ile Val Ser	
100 105 110	
ATG ACT TAT TCG GAG GTG CAA CAG GCC TGC AGA GCT CGT GGA ATG CGA	384
Met Thr Tyr Ser Glu Val Gln Gln Ala Cys Arg Ala Arg Gly Met Arg	
115 120 125	
GCT TAT GGT ATG CCT GAA CAT AGG TTG AGG AGG CAA TTG GAA GAC TGG	432
Ala Tyr Gly Met Pro Glu His Arg Leu Arg Arg Gln Leu Glu Asp Trp	
130 135 140	
ATT AAT TTA AGC TTG AAT GAA AAG GTT CCA CCA TCA TTA TTG CTT TTG	480
Ile Asn Leu Ser Leu Asn Glu Lys Val Pro Pro Ser Leu Leu Leu Leu	
145 150 155 160	
TCA AGG GCG CTG ATG TTG CCC GAG AAT GTT CCA GTG TCT GAT AAA CTT	528
Ser Arg Ala Leu Met Leu Pro Glu Asn Val Pro Val Ser Asp Lys Leu	
165 170 175	
AAA GCA ACA ATA AAT GCT CTT CCT GAA ACT ATT GTA ACT CAG ACA AAG	576
Lys Ala Thr Ile Asn Ala Leu Pro Glu Thr Ile Val Thr Gln Thr Lys	
180 185 190	
GCT GCT ATT GGA GAA AGA GAA GGA AAG ATT GAC AAT AAG ACC AAA ATT	624
Ala Ala Ile Gly Glu Arg Glu Gly Lys Ile Asp Asn Lys Thr Lys Ile	
195 200 205	
GAG GTC ATC AAA GAG GAA GAA CGC AAA ATT CGC GAA GAG CGC CAA GAA	672
Glu Val Ile Lys Glu Glu Glu Arg Lys Ile Arg Glu Glu Arg Gln Glu	
210 215 220	
GCA CGT GAG GAA GAG GAA CAA CGC AAG CAA GCC GAA CTT GCT CTT AAT	720
Ala Arg Glu Glu Glu Glu Gln Arg Lys Gln Ala Glu Leu Ala Leu Asn	
225 230 235 240	
GCC AGT TCT GCA GCA GCT GAG GCC TCT TCA GCT CAG GAA CTT TTG ATA	768
Ala Ser Ser Ala Ala Ala Glu Ala Ser Ser Ala Gln Glu Leu Leu Ile	
245 250 255	
GAT ACA GCT CCT GTA ATA GAT GCA GAA AAG ACA CCA AAG GTG GCA ACA	816
Asp Thr Ala Pro Val Ile Asp Ala Glu Lys Thr Pro Lys Val Ala Thr	
260 265 270	
TCA CCT GTT GAA TCA CCA TTG GCA CCA CCA GAA GTT CTG ATT ATG GGT	864
Ser Pro Val Glu Ser Pro Leu Ala Pro Pro Glu Val Leu Ile Met Gly	
275 280 285	
GCT CCT AAA ACA CCT GTT GCA ACC GAA GTG GAT AAG AAT GCT GAT GAG	912
Ala Pro Lys Thr Pro Val Ala Thr Glu Val Asp Lys Asn Ala Asp Glu	
290 295 300	
GTG GAA TTC ACC AAG AAA GAT CTT GAG GTT GTT GAA GAT GCA TTG GAT	960
Val Glu Phe Thr Lys Lys Asp Leu Glu Val Val Glu Asp Ala Leu Asp	
305 310 315 320	
ACA CTA TCG AAA GAC AAA AAT AAT TTG GTG ATT GAA AAG GAA GTT ATT	1008
Thr Leu Ser Lys Asp Lys Asn Asn Leu Val Ile Glu Lys Glu Val Ile	
325 330 335	

AAA GAC ATT AAG GAA GAA ATT GCT GAT TAC CAA GAA GAT GTA GAA GAA Lys Asp Ile Lys Glu Glu Ile Ala Asp Tyr Gln Glu Asp Val Glu Glu 340 345 350	1056
TTG AAA GAA GCC ATA GTT GCT GCT GAG AAA CCA AAG GAT GAG ATA AAA Leu Lys Glu Ala Ile Val Ala Ala Glu Lys Pro Lys Asp Glu Ile Lys 355 360 365	1104
GAA ACT AAA GGA GCT CAA CGA TTG TTG AAG AWG GTT AAC AAG ATG ATA Glu Thr Lys Gly Ala Gln Arg Leu Leu Lys Xaa Val Asn Lys Met Ile 370 375 380	1152
ACG AAA ATG GAT ACT GTT GTA CAA GAA ATT GAA AGC AAA GAA TCT GAG Thr Lys Met Asp Thr Val Val Gln Glu Ile Glu Ser Lys Glu Ser Glu 385 390 395 400	1200
AAG AAA GCC AAA ACA TTG CCA CTT GAA GCT CCT AGG AGC GCT ACT GAA Lys Lys Ala Lys Thr Leu Pro Leu Glu Ala Pro Arg Ser Ala Thr Glu 405 410 415	1248
ACT CAA GAA TTA GAT GTA AGG AAA GAA AGA GGA GAG ATT TTA ATT GAC Thr Gln Glu Leu Asp Val Arg Lys Glu Arg Gly Glu Ile Leu Ile Asp 420 425 430	1296
GAA TTA ATG GAC GCT ATT AAG AAA GTT AAA AAT GTG CCA GAC GAA AAT Glu Leu Met Asp Ala Ile Lys Lys Val Lys Asn Val Pro Asp Glu Asn 435 440 445	1344
CGC TTG AAA TTA ATT GAG AAC ATT TTG GGC AGG ATC GAT ACT GAC AAA Arg Leu Lys Leu Ile Glu Asn Ile Leu Gly Arg Ile Asp Thr Asp Lys 450 455 460	1392
GAT AGG CAT ATC AAA GTT GAA GAT GTA TTG AAG GTT ATT GAC ATT GTG Asp Arg His Ile Lys Val Glu Asp Val Leu Lys Val Ile Asp Ile Val 465 470 475 480	1440
GAA AAA GAA GAT GGT ATC ATG AGT ACA AAA CAA TTA GAT GAG TTG GTT Glu Lys Glu Asp Gly Ile Met Ser Thr Lys Gln Leu Asp Glu Leu Val 485 490 495	1488
CAG CTT TTG AAA AAG GAG GAA GTT ATT GAA TTG GAA GAA AAG AAA GAA Gln Leu Leu Lys Lys Glu Glu Val Ile Glu Leu Glu Glu Lys Lys Glu 500 505 510	1536
AAG CAA GAG TCT CAA CAG AAA AGT TTT GTA CCA CCA AGT GAA ACT TTG Lys Gln Glu Ser Gln Gln Lys Ser Phe Val Pro Pro Ser Glu Thr Leu 515 520 525	1584
CAT CTT GAA TCA TCA CAG CAG AAG AGT ACA GTT CCT AGC TCG GGA CAT His Leu Glu Ser Ser Gln Gln Lys Ser Thr Val Pro Ser Ser Gly His 530 535 540	1632
GAA GCT AAG GTG TCC GAA GAT GAC TTA AAT GTT AAA AAT AAA AAT TTG Glu Ala Lys Val Ser Glu Asp Asp Leu Asn Val Lys Asn Lys Asn Leu 545 550 555 560	1680
GAA GAA TCG ACC AAA ACT GAA TGT GGA GCA ATT GAC GAA GAG CAC AGA Glu Glu Ser Thr Lys Thr Glu Cys Gly Ala Ile Asp Glu Glu His Arg 565 570 575	1728
AGA GAG CAT TGC CAG TAC CCA GAC ATT ACA	1758

Arg Glu His Cys Gln Tyr Pro Asp Ile Thr
580 585

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Xaa = any amino acid
- (B) LOCATION: 379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

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Leu Glu Met Ala Lys Phe Leu Thr Glu Thr Leu Asp Asp Met Thr Leu
 1             5             10             15
Gln His Lys Asp His Arg Ser Glu Leu Ala Lys Glu Phe Ser Ile Trp
      20             25             30
Phe Thr Lys Met Arg Gln Ser Gly Ala Gln Ala Ser Asn Glu Glu Ile
      35             40             45
Met Lys Phe Ser Lys Leu Phe Glu Asp Glu Ile Thr Leu Asp Ser Leu
      50             55             60
Ala Arg Pro Gln Leu Val Ala Leu Cys Arg Val Leu Glu Ile Ser Thr
      65             70             75             80
Leu Gly Thr Thr Asn Phe Leu Arg Phe Gln Leu Arg Met Lys Leu Arg
      85             90             95
Ser Leu Ala Ala Asp Asp Lys Met Ile Gln Lys Glu Gly Ile Val Ser
      100            105            110
Met Thr Tyr Ser Glu Val Gln Gln Ala Cys Arg Ala Arg Gly Met Arg
      115            120            125
Ala Tyr Gly Met Pro Glu His Arg Leu Arg Arg Gln Leu Glu Asp Trp
      130            135            140
Ile Asn Leu Ser Leu Asn Glu Lys Val Pro Pro Ser Leu Leu Leu Leu
      145            150            155            160
Ser Arg Ala Leu Met Leu Pro Glu Asn Val Pro Val Ser Asp Lys Leu
      165            170            175
Lys Ala Thr Ile Asn Ala Leu Pro Glu Thr Ile Val Thr Gln Thr Lys
      180            185            190
Ala Ala Ile Gly Glu Arg Glu Gly Lys Ile Asp Asn Lys Thr Lys Ile
      195            200            205
Glu Val Ile Lys Glu Glu Glu Arg Lys Ile Arg Glu Glu Arg Gln Glu
      210            215            220

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Ala Arg Glu Glu Glu Glu Gln Arg Lys Gln Ala Glu Leu Ala Leu Asn
 225 230 235 240
 Ala Ser Ser Ala Ala Ala Glu Ala Ser Ser Ala Gln Glu Leu Leu Ile
 245 250 255
 Asp Thr Ala Pro Val Ile Asp Ala Glu Lys Thr Pro Lys Val Ala Thr
 260 265 270
 Ser Pro Val Glu Ser Pro Leu Ala Pro Pro Glu Val Leu Ile Met Gly
 275 280 285
 Ala Pro Lys Thr Pro Val Ala Thr Glu Val Asp Lys Asn Ala Asp Glu
 290 295 300
 Val Glu Phe Thr Lys Lys Asp Leu Glu Val Val Glu Asp Ala Leu Asp
 305 310 315 320
 Thr Leu Ser Lys Asp Lys Asn Asn Leu Val Ile Glu Lys Glu Val Ile
 325 330 335
 Lys Asp Ile Lys Glu Glu Ile Ala Asp Tyr Gln Glu Asp Val Glu Glu
 340 345 350
 Leu Lys Glu Ala Ile Val Ala Ala Glu Lys Pro Lys Asp Glu Ile Lys
 355 360 365
 Glu Thr Lys Gly Ala Gln Arg Leu Leu Lys Xaa Val Asn Lys Met Ile
 370 375 380
 Thr Lys Met Asp Thr Val Val Gln Glu Ile Glu Ser Lys Glu Ser Glu
 385 390 395 400
 Lys Lys Ala Lys Thr Leu Pro Leu Glu Ala Pro Arg Ser Ala Thr Glu
 405 410 415
 Thr Gln Glu Leu Asp Val Arg Lys Glu Arg Gly Glu Ile Leu Ile Asp
 420 425 430
 Glu Leu Met Asp Ala Ile Lys Lys Val Lys Asn Val Pro Asp Glu Asn
 435 440 445
 Arg Leu Lys Leu Ile Glu Asn Ile Leu Gly Arg Ile Asp Thr Asp Lys
 450 455 460
 Asp Arg His Ile Lys Val Glu Asp Val Leu Lys Val Ile Asp Ile Val
 465 470 475 480
 Glu Lys Glu Asp Gly Ile Met Ser Thr Lys Gln Leu Asp Glu Leu Val
 485 490 495
 Gln Leu Leu Lys Lys Glu Glu Val Ile Glu Leu Glu Glu Lys Lys Glu
 500 505 510
 Lys Gln Glu Ser Gln Gln Lys Ser Phe Val Pro Pro Ser Glu Thr Leu
 515 520 525
 His Leu Glu Ser Ser Gln Gln Lys Ser Thr Val Pro Ser Ser Gly His
 530 535 540
 Glu Ala Lys Val Ser Glu Asp Asp Leu Asn Val Lys Asn Lys Asn Leu

545 550 555 560

Glu Glu Ser Thr Lys Thr Glu Cys Gly Ala Ile Asp Glu Glu His Arg
 565 570 575

Arg Glu His Cys Gln Tyr Pro Asp Ile Thr
 580 585

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 293 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCCCGGCTGC AGGAATTCGG CACGAGATGA GAATGGAAAT GTGATTAGCT ATACTGATGA	60
AAATGGAAAC ATTATCAGTA CTACTGATGA GAATGGAAAT GTGATTAGCA TTACTGATGA	120
AAATGGAAAT GTGATTAGCA TTACTGATGA AAATGGAAAC ATTATCAGTA CTACTGATGA	180
GAATGGAAAT GTGATTAGCA TTACTGATGA AAATGGAAAT GTGATTAGCA TTACTGATGA	240
AAATGGAAAC ATTATTAGTA CTACTGATGA GAATGGAAAT GTGATTAGCA ATA	293

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTGGAAACAG CTATGACCAT GATTACCCCA AGCTCGAAAG TTAAVCCCTC ACTHARAGGG	60
GAACAAAAGT CTGGAGCTCC ACCCGCGGAT GCGGCCGCB TCTAGAACCT AGTGGACTCC	120
CCCCGSGCTG CAGGAATTCG GGCACGAGCT CCAGCTAGCC ATATACATTC ATCCAAAATG	180
AAGTTGSAAT GTGTCCTACC CGGCAACGGG ATGCCAGAAA TTGKTCGAA ATKTGTGGAC	240
GAGCACAAGC TTCGTGTCTK TCTATGAAAA ACGTATGGGA GCAGAAGTCG AGGGCCGACA	300
TCCTCGGCGA TGAATGGARA GGTATGTGC TCCGA	335

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATAGCTTTTA ATATTTTAA TTGATGTATT GCTCAATGGT GATTTCTGTT TATTAAGT 60
AGTTACCAAT ATGCTCGCTT CAATAGACAT AGCAAATGAA AGCATTCCGT ATCCTCAAGC 120
GTTACCAAAC TAACATTAAG GAGTTAAATA AATGTTGTTT CCAATAAATA TAATGGGAAA 180
AACATTTAAT ATTTGTCCA ATTTGTATTT ATTTTACTA CAATTATATA CAATAAATA 240
TTTTTATATA TATTTTATAA AGTTTATGAT GCAGGAGAGA AAATAATGTT AAGAATATAG 300
GTAATGTGTA TATATAAATG TTTGACAAGC ATGTTCTAGT TAAATAATAA ATACAATGTT 360
AAATCTACTT AAAAAAAAAA AAAAAAAAAA AAAAAA 396

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGAAAGCGAA GAATGAAAAG GGGAAACAAA AAAAGAAAAG ACGAAGGAGT GGAGAGATAA 60
AACGGAGGCA AAGAAGAAAA TGAGGATGCA AAAGAAAGGT AATAAAGAG ATGAAAAGAA 120
GGAAAAGGA AATAAGAAAG AAAGAGTGAG GGAAAATAA AGACAGAGGC GAAGCAAAAA 180
AGGAGGAGAA ATAGAGATTA AAAAGAAAT ACAGCGAAGA AACCAGGAAA GCGATAAAGA 240
AAAAAAAGA AAAAAGAGA GCAGTGAAAA AAAAAAAAAA AAAAA 285

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CAGATATTTA CTAAAYATTG TGAAAYAAAT CATTTTCAAA ATGGTSTCCA AAGTGTGTTG 60
TGCTCTTGCC ATCAATGGCT TTATAGGGGG CTSCACAAGY CTTTTTTCGA ACAAGATGMC 120
GTCTTAGATA ASATSGTAGA TRACATCTCT GRCTSMATAT GAGAACARCA TTGSMAGAAT 180
TAGCCAAGGR TNGCRAAATT GATATGMTTS CYGCTGTAAT TCGAAAAA 228

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CTT CGT GTC AAC CGC TGG GTC AGA CCT GTT ATT GCT ATG CAC CCA ACC	48
Leu Arg Val Asn Arg Trp Val Arg Pro Val Ile Ala Met His Pro Thr	
1 5 10 15	
ATG ACT CTT GCT GAA CGT CTC GGC AAA AAA GCT TTG CGC GAC CAA TAT	96
Met Thr Leu Ala Glu Arg Leu Gly Lys Lys Ala Leu Arg Asp Gln Tyr	
20 25 30	
GCT CCC GTT TGC TCC ATT GGA CAA CGT AAC ATC AAC ACC TTT GAC AAC	144
Ala Pro Val Cys Ser Ile Gly Gln Arg Asn Ile Asn Thr Phe Asp Asn	
35 40 45	
ATG ACC TTC CCC GCT CAA TTC GGA AAA TGC TGG CAC GCT TTG TTG CAA	192
Met Thr Phe Pro Ala Gln Phe Gly Lys Cys Trp His Ala Leu Leu Gln	
50 55 60	
ACT GTT CCC CAA AAG TAT TCC GAA GAA CGT GAA TAC AGC GAA GAA CAA	240
Thr Val Pro Gln Lys Tyr Ser Glu Glu Arg Glu Tyr Ser Glu Glu Gln	
65 70 75 80	
CAA TAC GAC CGT CAA ATG TCC GTC CTC GTT CGT GAA AAC GGC GAA GAA	288
Gln Tyr Asp Arg Gln Met Ser Val Leu Val Arg Glu Asn Gly Glu Glu	
85 90 95	
AAA AGA CGT TAT GAT TGT CTT GGG CAA CCG TTA CAA CAA TTG AAT TGC	336
Lys Arg Arg Tyr Asp Cys Leu Gly Gln Pro Leu Gln Gln Leu Asn Cys	
100 105 110	
AAT	339
Asn	

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Leu Arg Val Asn Arg Trp Val Arg Pro Val Ile Ala Met His Pro Thr
1 5 10 15

Met Thr Leu Ala Glu Arg Leu Gly Lys Lys Ala Leu Arg Asp Gln Tyr
20 25 30

Ala Pro Val Cys Ser Ile Gly Gln Arg Asn Ile Asn Thr Phe Asp Asn
35 40 45

Met Thr Phe Pro Ala Gln Phe Gly Lys Cys Trp His Ala Leu Leu Gln
50 55 60

Thr Val Pro Gln Lys Tyr Ser Glu Glu Arg Glu Tyr Ser Glu Glu Gln
65 70 75 80

Gln Tyr Asp Arg Gln Met Ser Val Leu Val Arg Glu Asn Gly Glu Glu
85 90 95

Lys Arg Arg Tyr Asp Cys Leu Gly Gln Pro Leu Gln Gln Leu Asn Cys
100 105 110

Asn

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 493 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TCC AGC TCC TCC AGC TCC AGC AGT GAC TCT TCC AGC TCC AGC AGC TCT	48
Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Ser Ser Ser Ser Ser	
1 5 10 15	
TCC TCT TCC AGC TCC AGC AGC TCC TCT TCT GAA TCT TCC GAA GAA AAA	96
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Glu Ser Ser Glu Glu Lys	
20 25 30	
ACC TCC CAC AAA AAA TCC GAA AAG AAG GAA CAC AAA TCC TGC TCC ATC	144
Thr Ser His Lys Lys Ser Glu Lys Lys Glu His Lys Ser Cys Ser Ile	
35 40 45	
AAG AAG CAA GTA CAA TTC GTA GAA AAA GAC GGT AAA CTC TGC TTC AGC	192
Lys Lys Gln Val Gln Phe Val Glu Lys Asp Gly Lys Leu Cys Phe Ser	
50 55 60	
ATC CGT CCC TTG GCC GCT TGC CAA AAA CAC TGC AAA GCC ACT GAA ACC	240
Ile Arg Pro Leu Ala Ala Cys Gln Lys His Cys Lys Ala Thr Glu Thr	
65 70 75 80	
ACT CAA ATG GAA GTC GAA GTA TAC TGC CCC TCT GGC AGC CTT GCT GAA	288
Thr Gln Met Glu Val Glu Val Tyr Cys Pro Ser Gly Ser Leu Ala Glu	
85 90 95	

CTT TAC AAA CAA AAG ATC CTT AAG GGA GCC AAC CCC GAC TTG AGC GAC 336
 Leu Tyr Lys Gln Lys Ile Leu Lys Gly Ala Asn Pro Asp Leu Ser Asp
 100 105 110

AAG ACT CCT TCC AGA ATC TTG AAA TTC AAG GTT CCC AAA GCT TGC ACC 384
 Lys Thr Pro Ser Arg Ile Leu Lys Phe Lys Val Pro Lys Ala Cys Thr
 115 120 125

GCT TAC TAAATCTGAA ATAAATTACA TGGATTAGTT CATTTCTGAT GTAGTGCAAT 440
 Ala Tyr
 130

TAGTTCGATA ATAAATTATT CAATGAGCAT TTAAAAA AAAA AAAAA AAC 493

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Ser Ser Ser Ser Ser
 1 5 10 15
 Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Glu Ser Ser Glu Glu Lys
 20 25 30
 Thr Ser His Lys Lys Ser Glu Lys Lys Glu His Lys Ser Cys Ser Ile
 35 40 45
 Lys Lys Gln Val Gln Phe Val Glu Lys Asp Gly Lys Leu Cys Phe Ser
 50 55 60
 Ile Arg Pro Leu Ala Ala Cys Gln Lys His Cys Lys Ala Thr Glu Thr
 65 70 75 80
 Thr Gln Met Glu Val Glu Val Tyr Cys Pro Ser Gly Ser Leu Ala Glu
 85 90 95
 Leu Tyr Lys Gln Lys Ile Leu Lys Gly Ala Asn Pro Asp Leu Ser Asp
 100 105 110
 Lys Thr Pro Ser Arg Ile Leu Lys Phe Lys Val Pro Lys Ala Cys Thr
 115 120 125
 Ala Tyr
 130

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTAGTGCCAT CATTGCTAAA CSTTYTGACG GTKGGGCGCT GTATWGGTGC TGCCTGGAAA 60
TTGCATCGAT GCACTWCCGT GTCGGGCGCA WATAGTGCKK TGGSCCCTGT CTGMTTATAG 120
ACATTCAGGG CGCSGGS AKT AGCCATGTTT ATGGCTCMCA AWMTGCATTC ACAGTGGGGT 180
CACATTTTCTAG TCGCATGATT KMTCAARTTA GTATMWGADA TATATTTTTC TCATACTAAG 240
TAGTGAGCDA ATAACACGCG ARWWACRAAC ACCGAATATC TTKAGTTTTT GCACAGATAT 300
KTGTAA 306

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACCGGATACG TTGCCAATGA CTACGTCACC ACCAATGTTG TTTCCACTCC AGTTACTGGA 60
TACACCACCG GACATCTTGC TAATGACTAC GTCACCACCA ATGTTGTATC CACTCCAGTT 120
ACTGGATACA CCACCGGACA TCTTGCCAAT GACTACGTCA CCACCAACGT AGTTTCCGCA 180
CCAGTCACCA CTGGATACAC CACTGGCTAT ACCACCGGTA ATGTCGGATA CACCACCGGA 240
GTTACTGGTT ACACCAACCG AGTTAGTGGA TATACCAATG GACTTAATGG TTATACCACT 300
GGTAGCTATG TCAGCTCCCC AGGATACACT TCTTCTGGAC TTGTCAACGT TTTCTAGATT 360
TATGATTTCG TCTGCCCTCA ATGATGATGA CCACACTTTT TACTTTTAT GATATTTGGA 420
AAAAATAAAT AACTGGAAGA ATATATAATA ATTTCAAAT AAAAAAAAAA AAAAAAAAAA 480
CTCGAGGGGG 490

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AAAAAATCGA AAGAAGGCGT AAAACCAAAA TGGGCACAGA AGGATATTCG GGATTTTAGT 60
GATGCCGACA TGGAGAGGTT ACTGGATCAA TGGGAAGAAG ATGAAGACCC CCTTCCAGAA 120

GACGAATTGC CCGAACATCT CAGACCTGAT CCAAAGATCG ACATAAGCAA CATCGATATG 180
 AGCAATCCCB AAAACATACT AAAGGCTTCC AAAAAAGGCA AGACTTTGAT GGCATTCGTA 240
 CAAGTCAGTG GAAATCCAAC ACAAGAAGAA GCCGAAACCA TCACTAAATT GTGGCAAGGC 300
 AGTCTATGGA ATAGTCATAT ACAAGCCGAA AGATATATGG TTAGCGATGA CAGGGCTATA 360
 TTTATGTTTA AAGATGGTTC TCAAGCTTGG CCTGCTAAAG ACTTTTTAGT GGAACAAGAA 420
 AGGTGTAAAG ATGTTACAAT TGAAAATAAA ATATATCCTG GTAAATATTC TTCGACTAAA 480
 GAAGAATTAT AATATAATAT ATTATAATTA TAATCTATAA AATAGATTTG AAATTCTACA 540
 TTCATGATCT ACTATGTATG ATATTAATTT ATTAAAAATA ATGTTTTTTC AAGTAAAAAA 600
 AAAAAAAAAA AAAAAA 616

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 475 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTCGTGCGGG ACAGATATAG GACCGGATTC GTTAATTGAT TTGAGTGAAG TGGCTTCTGG 60
 TGGTTCTGAT ATTGACACAA AATTTTCCAA TTTAAAAATA GATAAAAAGC CTGTTGCAAC 120
 TTCACAACAA GGAATTGATG AATTTGATAT GTTTCACAA TCGAGAAACA TTTCTAGTGA 180
 GGGATCAACC AGTGCTATGA AGGAAGGACA CGGTTTGGAC TTATTATCAA ATACACATAA 240
 AAATGTACCA CCAACAATTC CACAAGCCGG ACAACTTCCA AGGGATTCTG AGTTTGATGA 300
 AATTGCTGCT TGGCTTGATG AAAAGGTTGA AGACAAAGCC CAAGTTCCCG AAGACAGTAT 360
 TACAAGCAGT GAATTTGATA AATTCCTGGC AGAACGGGCA GCTGTTGCTG AAACCTTGCC 420
 AAATATTCCA CCGACTACAC AAAGTAATCA TTCAAATATT GAAGCAAACG ATAAA 475

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCGGCACGGG AGGTAGTGAC GAAAAATAAC GATACGGGAC TCATCCGAGG CCCCCTAATC 60
 GGAATGAGTA CACTTTAAAT CCTTTAACGA GGATCTATTA GAGGGCCAGT CTGTGTGCCA 120

GCAGCCGCGG TAATTCCAGC TCTAATAGCG TATATTAAAG TTGTTGCGGT TAAAAAGCTC 180
GTAGTTGAAT CTGTGTCCCA CACTGTYGGT TCACCGCTCG CGGTGTTCAA CTGGCATGTC 240
TGTGGGACGT CCTACCGGTG GGCTTAGCCC GTCAAAGGC GGCCCAACTC AAAAT 295

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CTGACTAATC CCAGGACTCC TTTATCCTGT TTGCGCAATG TCGATACCCA TCTCACAATG 60
GTTAATGATT TATCGGCTAA ACAGAAGAGT CCTAAGAAGG TTGTTAAAGG TGTCTCTAGA 120
ATACCGACTT TTAGACCCAA GGCTATGAAT GCTGATGTTG AGAATTTTGA TTCGATGAGG 180
TGCGATGTTT GGRACAAAGA CACCAGTGTG GTTATATAAT TACTAAAGCA ATCCACATGT 240
AGCTAATTTT TTTTTCACAA TTTTATTGTG AACTATGTGT ATTTATATGA ATTCTTGTGG 300
AATATAATTT TAAGTTTTTA AATGAAATAT AGATATTATT CTAAAAAAAA AAAACAAAAA 360
AAAAAAAAAA AA 372

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGATTCGGCA CGACAATTTA TTAAGCGCAT TATTTGCAAG TGTAATTTGC TCCTTTAACG 60
CGGAAGTACA AAATCGAATC GTTGGTGGCA ATGATGTAAG TATTTCAAAA ATTGGGTGGC 120
AAGTATCTAT TCAAAGTAAT AACCAACATT TCTGTGGTGG TTCAATCATT GCTAAAGATT 180
GGGTACTGAC TTCTTCTCAA TCGTCTGTGG ACAAACAAAG TCCACCGAAG GATTTAACTG 240
TTCGTGTTGG AA 252

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 613 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATTCCTGCTG TTAATAGTAC TAATGCAGTA ATTGCTGCHA GCTGCTGCAC AGAGGTTTTT 60
AAAATGGCAA CAAGTTGTTA CACCCACATG AACAACTACA TGGTATTCAA TGATACCGAT 120
GGGATTTATA CATATACTTA CGAAGCTGAA AGAAAACCTG ACTGTTTAGC TTGTTACAAA 180
ATTCCAAAAA CTATAGAAGT TTCTAATCCT GAAATATGA CTCTCCAAGA CTTGATTACT 240
TTGTTGTGTG AAGGGGCTGA ATATCAAATG AAGAGCCCAG GTATTGTAGC CTCAATCGAA 300
GGCAAAAACA AAACCTTATA CATGTCAACA GTAGCAAGTA TAGAAGAAAA GACTAAACAG 360
AATCTAACAA AGTCTCTAAA AGAATTAAAT CTAGAAAATG GAATGGAACT GATGGTTGCA 420
GATGTGACGA CACCAAACAC AATATTACTT AAATTAAAT ATAAGAATGT AATTGAAAAC 480
GATGTTGAGA TGAAGTGATA TTTACTTAAA AATGTTATCT TACAATAATT GATAATTTAT 540
ATTTAATACT TTTGGAAGTT TGTATTTAAT GATAATAAAT TATTATAAGA ATTAAAAAAA 600
AAAAAAAAAA AAA 613

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TT GAT ATT TGC TCT GTT GAG GGT GCC TTA GGA TTT TTA GTG GAA ATG 47
Asp Ile Cys Ser Val Glu Gly Ala Leu Gly Phe Leu Val Glu Met
1 5 10 15
TTA AAA TAT AAG GCC CCA AGT AAA ACT CTA GCT ATT GTA GAG AAT GCT 95
Leu Lys Tyr Lys Ala Pro Ser Lys Thr Leu Ala Ile Val Glu Asn Ala
20 25 30
GGT GGA ATA TTA CGA AAT GTA TCT AGT CAT ATA GCC CTT AGA GAG GAC 143
Gly Gly Ile Leu Arg Asn Val Ser Ser His Ile Ala Leu Arg Glu Asp
35 40 45
TAC AGA GAA ATA CTT CGA CAT CAT AAT TGC TTA ACA ATA TTA CTA CAA 191
Tyr Arg Glu Ile Leu Arg His His Asn Cys Leu Thr Ile Leu Leu Gln
50 55 60
CAA TTA AAA TCA CCA AGC CTC ATA ATT GTC AGT AAT GCT TGT GGG ACA 239

Gln Leu Lys Ser Pro Ser Leu Ile Ile Val Ser Asn Ala Cys Gly Thr
65 70 75

TTA TGG AAT TTA TCT GCT AGG AAT TCA ACA GAT CAA CAA TTT TTA TGG 287
Leu Trp Asn Leu Ser Ala Arg Asn Ser Thr Asp Gln Gln Phe Leu Trp
80 85 90 95

GAG AAT GGT GCT GTC CCT TTA TTA AGA AGT TTG ATA TAT TCT AAG CAT 335
Glu Asn Gly Ala Val Pro Leu Leu Arg Ser Leu Ile Tyr Ser Lys His
100 105 110

AAA ATG ATA TCT ATG GGA TCA AGT GCA GCT CTC AAA AAT TTG TTA AAT 383
Lys Met Ile Ser Met Gly Ser Ser Ala Ala Leu Lys Asn Leu Leu Asn
115 120 125

GCA AAA CCT GAG TGC ATC AAT TTC TTA AGT GAT TCT TCT TCT AAA GGA 431
Ala Lys Pro Glu Cys Ile Asn Phe Leu Ser Asp Ser Ser Ser Lys Gly
130 135 140

GTT CCA AAT CTA ACT ACA TTG GGT GTA AGA AAA CAA AAA TCT CTA CAT 479
Val Pro Asn Leu Thr Thr Leu Gly Val Arg Lys Gln Lys Ser Leu His
145 150 155

GAG TTA ATA GAT CAA AAT CTT TCA GAA ACT TGT GAT AAT ATA GAT AGT 527
Glu Leu Ile Asp Gln Asn Leu Ser Glu Thr Cys Asp Asn Ile Asp Ser
160 165 170 175

GTG GCC GCT AA 538
Val Ala Ala

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Asp Ile Cys Ser Val Glu Gly Ala Leu Gly Phe Leu Val Glu Met Leu
1 5 10 15

Lys Tyr Lys Ala Pro Ser Lys Thr Leu Ala Ile Val Glu Asn Ala Gly
20 25 30

Gly Ile Leu Arg Asn Val Ser Ser His Ile Ala Leu Arg Glu Asp Tyr
35 40 45

Arg Glu Ile Leu Arg His His Asn Cys Leu Thr Ile Leu Leu Gln Gln
50 55 60

Leu Lys Ser Pro Ser Leu Ile Ile Val Ser Asn Ala Cys Gly Thr Leu
65 70 75 80

Trp Asn Leu Ser Ala Arg Asn Ser Thr Asp Gln Gln Phe Leu Trp Glu
85 90 95

Asn Gly Ala Val Pro Leu Leu Arg Ser Leu Ile Tyr Ser Lys His Lys

100	105	110
Met Ile Ser Met Gly Ser Ser Ala Ala Leu Lys Asn Leu Leu Asn Ala		
115	120	125
Lys Pro Glu Cys Ile Asn Phe Leu Ser Asp Ser Ser Ser Lys Gly Val		
130	135	140
Pro Asn Leu Thr Thr Leu Gly Val Arg Lys Gln Lys Ser Leu His Glu		
145	150	155
Leu Ile Asp Gln Asn Leu Ser Glu Thr Cys Asp Asn Ile Asp Ser Val		
165	170	175
Ala Ala		

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 1..388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTT CTT CTT AAA CAG TTG GAC TCT GGA TTG TTA CTT GTT ACA GGT CCC	48
Val Leu Leu Lys Gln Leu Asp Ser Gly Leu Leu Leu Val Thr Gly Pro	
1 5 10 15	
TTC TTA ATC AAT GCA TGC CCA TTG CGT CGC ATT TCC CAA AAC TAT GTC	96
Phe Leu Ile Asn Ala Cys Pro Leu Arg Arg Ile Ser Gln Asn Tyr Val	
20 25 30	
ATT GCC ACC TCT ACC CGA TTA GAC GTT AGT GGA GTT AAA TTA CCA GAA	144
Ile Ala Thr Ser Thr Arg Leu Asp Val Ser Gly Val Lys Leu Pro Glu	
35 40 45	
CAC ATC AAT GAT GAT TAT TTC AAA AGG CAA AAG AAC AAG CGT GCA AAG	192
His Ile Asn Asp Asp Tyr Phe Lys Arg Gln Lys Asn Lys Arg Ala Lys	
50 55 60	
AAA GAG GAA GGT GAT ATT TTT GCT GCC AAG AAA GAG GCT TAT AAA CCA	240
Lys Glu Glu Gly Asp Ile Phe Ala Ala Lys Lys Glu Ala Tyr Lys Pro	
65 70 75 80	
ACT GAG CAA AGG AAG AAT GAC CAA AAG CTT GTA GAC AAA ATG GTT TTA	288
Thr Glu Gln Arg Lys Asn Asp Gln Lys Leu Val Asp Lys Met Val Leu	
85 90 95	
GGA GTA ATC AAG AAG CAC CCA GAC CAC AAA CTT TTG TAT ACA TAT TTG	336
Gly Val Ile Lys Lys His Pro Asp His Lys Leu Leu Tyr Thr Tyr Leu	
100 105 110	

TCA GCT ATG TTT GGT TTG AAA TCT TCC CAA TAT CCA CAT CGT ATG AAG 384
 Ser Ala Met Phe Gly Leu Lys Ser Ser Gln Tyr Pro His Arg Met Lys
 115 120 125

TTC T AAATACTATA TTCATAAAAT AAATTGAACT TCTCAAAAAA AAAA 432
 Phe

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Val Leu Leu Lys Gln Leu Asp Ser Gly Leu Leu Leu Val Thr Gly Pro
 1 5 10 15
 Phe Leu Ile Asn Ala Cys Pro Leu Arg Arg Ile Ser Gln Asn Tyr Val
 20 25 30
 Ile Ala Thr Ser Thr Arg Leu Asp Val Ser Gly Val Lys Leu Pro Glu
 35 40 45
 His Ile Asn Asp Asp Tyr Phe Lys Arg Gln Lys Asn Lys Arg Ala Lys
 50 55 60
 Lys Glu Glu Gly Asp Ile Phe Ala Ala Lys Lys Glu Ala Tyr Lys Pro
 65 70 75 80
 Thr Glu Gln Arg Lys Asn Asp Gln Lys Leu Val Asp Lys Met Val Leu
 85 90 95
 Gly Val Ile Lys Lys His Pro Asp His Lys Leu Leu Tyr Thr Tyr Leu
 100 105 110
 Ser Ala Met Phe Gly Leu Lys Ser Ser Gln Tyr Pro His Arg Met Lys
 115 120 125
 Phe

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 47..313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ser Gln Cys Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr
65 70 75 80

Arg Pro Asn Gln Lys His Cys Tyr Cys
85

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 595 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TTTTTTTTTT TTTTTTTTTT TTTTCAACTT TTGCAATTCA GTTTATATAA TTCTTATAAA	60
TATTAGACAA TGTTACAATA TTTATAATAA TCTATTTGTA AACATTCAGT ATTTCTTGAA	120
CATTTTGTTA CGGTACGGTA AGTCCCAGC AATTTGCTGT TAAAATAAAT TGGAGGCAAA	180
ACATGTTAGG ATCATTGAAA ACTTCAAAAT TTTATGATTG CTATCTAGCA TAATTTTAGT	240
AATTTATATC AATTTGGTCT TTCATCCGGA ATATGGTTAT TCGCAATAAC AGTGTTTTTG	300
ATTTGGTCGT GTTGAACCAC CGTTCCACA AGCACCACCT CCAAATCCAC ATTGACTTTT	360
GCAAAATATT TTGCAACTTT GATGATTTCC AATACAAAA TCTTCAATAG TAAGCTTCCC	420
AGATGGTATT GACACCTCTT TTGTAATTGG ATTATTTCTT CCCGATTAC ACTTTTCAGT	480
GACCATTTTT GACATAGATA CTTGATTTAA TAAACACAC AACACGCAA TTGCCAGTAA	540
AAATTCATA TCGAATTGA AAAATTTAAT GTTAAACAA AATATTGAAT TTCCA	595

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ATG AAA TTT TTA CTG GCA ATT TGC GTG TTG TGT GTT TTA TTA AAT CAA	48
Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln	
1 5 10 15	
GTA TCT ATG TCA AAA ATG GTC ACT GAA AAG TGT AAA TCG GGA GGA AAT	96
Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn	

20	25	30	
AAT CCA AGT ACA AAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT			144
Asn Pro Ser Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile			
35	40	45	
GAA GAT TTT TGT ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TGC AAA			192
Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys			
50	55	60	
AGT CAA TGT GGA TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA			240
Ser Gln Cys Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr			
65	70	75	80
CGA CCA AAT CAA AAA CAC TGT TAT TGC GAA			270
Arg Pro Asn Gln Lys His Cys Tyr Cys Glu			
85	90		

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln			
1	5	10	15
Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn			
20	25	30	
Asn Pro Ser Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile			
35	40	45	
Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys			
50	55	60	
Ser Gln Cys Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr			
65	70	75	80
Arg Pro Asn Gln Lys His Cys Tyr Cys Glu			
85	90		

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TTGCAATAA CAGTGT TTTT GATTGGTCG TGTTGAACCA CCGTTTCCAC AAGCACCACC	60
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TCCAAATCCA CATTGACTTT TGCAAAATAT TTTGCAACTT TGATGATTTT CAATACAAAA 120
 ATCTTCAATA GTAAGCTTCC CAGATGGTAT TGACACCTCT TTTGTACTTG GATTATTTCC 180
 TCCCAGATTTA CACTTTTCAG TGACCATTTT TGACATAGAT ACTTGATTTA ATAAAACACA 240
 CAACACGCAA ATTGCCAGTA AAAATTTTCAT 270

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TCA AAA ATG GTC ACT GAA AAG TGT AAA TCG GGA GGA AAT AAT CCA AGT 48
 Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser
 1 5 10 15
 ACA AAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT GAA GAT TTT 96
 Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe
 20 25 30
 TGT ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TGC AAA AGT CAA TGT 144
 Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys Ser Gln Cys
 35 40 45
 GGA TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA CGA CCA AAT 192
 Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr Arg Pro Asn
 50 55 60
 CAA AAA CAC TGT TAT TGC GAA 213
 Gln Lys His Cys Tyr Cys Glu
 65 70

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser
 1 5 10 15
 Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe
 20 25 30

Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys Ser Gln Cys
 35 40 45
 Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr Arg Pro Asn
 50 55 60
 Gln Lys His Cys Tyr Cys Glu
 65 70

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TTCGCAATAA CAGTGTITTTT GATTGGTCG TGTTGAACCA CCGTTTCCAC AAGCACCACC 60
 TCCAAATCCA CATTGACTTT TGCAAAATAT TTTGCAACTT TGATGATTTC CAATACAAAA 120
 ATCTTCAATA GTAAGCTTCC CAGATGGTAT TGACACCTCT TTTGTACTTG GATTATTTCC 180
 TCCCGATTTA CACTTTTCAG TGACCATTTT TGA 213

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1007 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TGG AAA GTT AAT AAA AAA TGT ACA TCA GGT GGA AAA AAT CAA GAT AGA 48
 Trp Lys Val Asn Lys Lys Cys Thr Ser Gly Gly Lys Asn Gln Asp Arg
 1 5 10 15
 AAA CTC GAT CAA ATA ATT CAA AAA GGC CAA CAA GTT AAA ATC CAA AAT 96
 Lys Leu Asp Gln Ile Ile Gln Lys Gly Gln Gln Val Lys Ile Gln Asn
 20 25 30
 ATT TGC AAA TTA ATA CGA GAT AAA CCA CAT ACA AAT CAA GAG AAA GAA 144
 Ile Cys Lys Leu Ile Arg Asp Lys Pro His Thr Asn Gln Glu Lys Glu
 35 40 45
 AAA TGT ATG AAA TTT TGC AAA AAA GTT TGC AAA GGT TAT AGA GGA GCT 192
 Lys Cys Met Lys Phe Cys Lys Lys Val Cys Lys Gly Tyr Arg Gly Ala
 50 55 60

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TGT GAT GGC AAT ATT TGC TAC TGC AGC AGG CCA AGT AAT TTA GGT CCT      240
Cys Asp Gly Asn Ile Cys Tyr Cys Ser Arg Pro Ser Asn Leu Gly Pro
 65              70              75              80

GAT TGG AAA GTA AGC AAA GAA TGC AAA GAT CCC AAT AAC AAA GAT TCT      288
Asp Trp Lys Val Ser Lys Glu Cys Lys Asp Pro Asn Asn Lys Asp Ser
      85              90              95

CGT CCT ACG GAA ATA GTT CCA TAT CGA CAA CAA TTA GCA ATT CCA AAT      336
Arg Pro Thr      100      105      110

ATT TGC AAA CTA AAA AAT TCA GAG ACC AAT GAA GAT TCC AAA TGC AAA      384
Ile Cys Lys Leu Lys Asn Ser Glu Thr Asn Glu Asp Ser Lys Cys Lys
      115              120              125

AAA CAT TGC AAA GAA AAA TGT CGT GGT GGA AAT GAT GCT GGA TGT GAT      432
Lys His Cys Lys Glu Lys Cys Arg Gly Gly Asn Asp Ala Gly Cys Asp
      130              135              140

GGA AAC TTT TGT TAT TGT CGA CCA AAA AAT AAA TAATAATTAT AATAAATAAA      485
Gly Asn Phe Cys Tyr Cys Arg Pro Lys Asn Lys
      145              150              155

TTGTTATAGT TATTAGTTAT CCCATCACAT ATTAGAAAAG TGGCTTATAA TTTATGAACA      545

ATATAACACA TAAATTAGTT GTGTAATTC GAATGTTTTT TTCAAATATA AGGCGTTTTT      605

CTAGAATATC TTGATATTAG AAACAACTT AGATTATTTT GTTGTGTATA AAATATTCAA      665

ATACGTAAGT TATATTGAAC AAAGCATTTA GAAGCTACAT TAGATATACT AAATAAGTGC      725

AAAATTGCAT GGAAACCCTT ACTGGATTTA CTACATATTT TCTTCCTAAA TATTGTCTTG      785

GTATTACTCT TATTATATAA AAATTAATAT AAAATTGTAG ACAGAGACGA ATTGGGGTAT      845

TGTTATATAT AAAAAAGTAG TGGATTATTT AATTCTAAAA AAGTTTGCAA AATGTTTCAT      905

ACATAATAAC CGAATATTTT CAAATATATA AATATTGTAA TGAATAAATG CGCATCTGTA      965

TGCTTAATAT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA      1007

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(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

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Trp Lys Val Asn Lys Lys Cys Thr Ser Gly Gly Lys Asn Gln Asp Arg
  1              5              10              15

Lys Leu Asp Gln Ile Ile Gln Lys Gly Gln Gln Val Lys Ile Gln Asn
      20              25              30

Ile Cys Lys Leu Ile Arg Asp Lys Pro His Thr Asn Gln Glu Lys Glu

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35

40

45

Lys Cys Met Lys Phe Cys Lys Lys Val Cys Lys Gly Tyr Arg Gly Ala
50 55 60

Cys Asp Gly Asn Ile Cys Tyr Cys Ser Arg Pro Ser Asn Leu Gly Pro
65 70 75 80

Asp Trp Lys Val Ser Lys Glu Cys Lys Asp Pro Asn Asn Lys Asp Ser
85 90 95

Arg Pro Thr Glu Ile Val Pro Tyr Arg Gln Gln Leu Ala Ile Pro Asn
100 105 110

Ile Cys Lys Leu Lys Asn Ser Glu Thr Asn Glu Asp Ser Lys Cys Lys
115 120 125

Lys His Cys Lys Glu Lys Cys Arg Gly Gly Asn Asp Ala Gly Cys Asp
130 135 140

Gly Asn Phe Cys Tyr Cys Arg Pro Lys Asn Lys
145 150 155

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1007 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTATATTAAG CATACAGATG CGCATTTTATT 60
CATTACAATA TTTATATATT TGAAAATATT CGGTTATTAT GTATGAAACA TTTTGCAAAC 120
TTTTTTAGAA TTAAATAATC CACTACTTTT TTATATATAA CAATACCCCA ATTCGTCTCT 180
GTCTACAATT TTATATTAAT TTTTATATAA TAAGAGTAAT ACCAAGACAA TATTTAGGAA 240
GAAAATATGT AGTAAATCCA GTAAGGGTTT CCATGCAATT TTGCACTTAT TTAGTATATC 300
TAATGTAGCT TCTAAATGCT TTGTTCAATA TAACTTACGT ATTTGAATAT TTTATACACA 360
ACAAAATAAT CTAAGTTAGT TTCTAATATC AAGATATTCT AGAAAAACGC CTTATATTTG 420
AAAAAAACAT TCGAAATTAC ACAACTAATT TATGTGTTAT ATTGTTTCATA AATTATAAGC 480
CACTTTTCTA ATATGTGATG GGATAACTAA TAACTATAAC AATTTATTTA TTATAATTAT 540
TATTTATTTT TTGGTCGACA ATAACAAAAG TTTCCATCAC ATCCAGCATC ATTTCCACCA 600
CGACATTTT CTTTGCAATG TTTTTCGCAT TTGGAATCTT CATTGGTCTC TGAATTTTTT 660
AGTTTGCAAA TATTTGGAAT TGCTAATTGT TGTCGATATG GAACTATTTC CGTAGGACGA 720
GAATCTTTGT TATTGGGATC TTTGCATTCT TTGCTTACTT TCCAATCAGG ACCTAAATTA 780

CTTGGCCTGC TGCAGTAGCA AATATTGCCA TCACAAGCTC CTCTATAACC TTTGCAAAC 840
 TTTTTCGAAA ATTTTCATACA TTTTCTTTC TCTTGATTG TATGTGGTTT ATCTCGTATT 900
 AATTTGCAAA TATTTTGGAT TTTAACTTGT TGGCCTTTTT GAATTATTG ATCGAGTTTT 960
 CTATCTTGAT TTTTCCACC TGATGTACAT TTTTATTAA CTTTCCA 1007

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..1062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCA GAA TTG AAA TTT GTG TTT GCG ACT GCA CGA GGT ATG TCA CAT ACA	48
Glu Leu Lys Phe Val Phe Ala Thr Ala Arg Gly Met Ser His Thr	
1 5 10 15	
CCT TGT GAT TAT CCA GGC GGT CCA AAA ATT ACA CAC AAG TCT GAA GAT	96
Pro Cys Asp Tyr Pro Gly Gly Pro Lys Ile Thr His Lys Ser Glu Asp	
20 25 30	
TCA AGC CAA TTG ACA CCG GCA GGT CAA GAA GAG GCA TTA AAA ATT GGC	144
Ser Ser Gln Leu Thr Pro Ala Gly Gln Glu Glu Ala Leu Lys Ile Gly	
35 40 45	
AAA TTA TTA TCC GAA CAT TAC AGA ACT AAT TTA AAA GTT GAC AAA TGG	192
Lys Leu Leu Ser Glu His Tyr Arg Thr Asn Leu Lys Val Asp Lys Trp	
50 55 60	
GAT TCA AAT AAA AAT TAT TGG ACA TTA GCT AGT GCT ACG AGA AGA TCT	240
Asp Ser Asn Lys Asn Tyr Trp Thr Leu Ala Ser Ala Thr Arg Arg Ser	
65 70 75	
CAA GAA GGA GCG CTT ATC ATT GGT TCT GGT CTA GAA GAA AAG GAA AAG	288
Gln Glu Gly Ala Leu Ile Ile Gly Ser Gly Leu Glu Glu Lys Glu Lys	
80 85 90 95	
GCA GTT TGG ACA AAA GAG AAA GGA GAT AAA ACC ATA TTT TCT TCG TTT	336
Ala Val Trp Thr Lys Glu Lys Gly Asp Lys Thr Ile Phe Ser Ser Phe	
100 105 110	
GGT GAA TAT GCT AAA TTT TAT AGT CCA AAA ACT TGT CCA AAC TTC ATA	384
Gly Glu Tyr Ala Lys Phe Tyr Ser Pro Lys Thr Cys Pro Asn Phe Ile	
115 120 125	
GCA CAA CAG AAA ATA GCA GTA AGA GAC TTG TTA ACA AAA AGT GCA AAA	432
Ala Gln Gln Lys Ile Ala Val Arg Asp Leu Leu Thr Lys Ser Ala Lys	
130 135 140	
GAT TAT AAA AAT TCA CTT GCA AAA TTA AAA GAA GCG TAT AAA ATA GAT	480

Asp Tyr Lys Asn Ser Leu Ala Lys Leu Lys Glu Ala Tyr Lys Ile Asp	
145 150 155	
GCG ACG ACA AGC CCT CAG AAT GTT TGG CTG GCA TAT GAA ACT TTG AAT	528
Ala Thr Thr Ser Pro Gln Asn Val Trp Leu Ala Tyr Glu Thr Leu Asn	
160 165 170 175	
TTA CAA AGC AAG CAA AAT AAC GCT CCA ACA TGG TGG AAT ACT GTA AAC	576
Leu Gln Ser Lys Gln Asn Asn Ala Pro Thr Trp Trp Asn Thr Val Asn	
180 185 190	
AAA GAT CTA AAA CAA TTC TCT GAG AAA TAT TTA TGG ACC GCC TTG ACT	624
Lys Asp Leu Lys Gln Phe Ser Glu Lys Tyr Leu Trp Thr Ala Leu Thr	
195 200 205	
TCT AAT GAT AAT CTT AGA AAG ATG TCA GGA GGT CGT ATG ATT AAC GAT	672
Ser Asn Asp Asn Leu Arg Lys Met Ser Gly Gly Arg Met Ile Asn Asp	
210 215 220	
ATA TTG AAC GAT ATC GAA AAC ATA AAG AAA GGA GAG GGA CAA CCG GGT	720
Ile Leu Asn Asp Ile Glu Asn Ile Lys Lys Gly Glu Gly Gln Pro Gly	
225 230 235	
GCT CCA GGA GGA AAG GAA AAC AAA TTA TCA GTG CTG ACC GTT CCT CAA	768
Ala Pro Gly Gly Lys Glu Asn Lys Leu Ser Val Leu Thr Val Pro Gln	
240 245 250 255	
GCT ATC TTA GCA GCA TTT GTT TCA GCA TTT GCT CCC GAA GGT ACA AAA	816
Ala Ile Leu Ala Ala Phe Val Ser Ala Phe Ala Pro Glu Gly Thr Lys	
260 265 270	
ATT GAA AAT AAG GAC CTT GAT CCG TCT ACT TTA TAT CCT GGC CAA GGA	864
Ile Glu Asn Lys Asp Leu Asp Pro Ser Thr Leu Tyr Pro Gly Gln Gly	
275 280 285	
GCA CTT CAC GTT ATT GAA CTA CAC CAA GAT AAG AGC GAT TGG AGC ATA	912
Ala Leu His Val Ile Glu Leu His Gln Asp Lys Ser Asp Trp Ser Ile	
290 295 300	
AAA GTT CTC TAT AGA AAC AAT GAC CAA ATG AAG CTG AAA CCA ATG AAA	960
Lys Val Leu Tyr Arg Asn Asn Asp Gln Met Lys Leu Lys Pro Met Lys	
305 310 315	
CTT GCA CAA TGC GGT GAC AAG TGT TCT TAT GGT ACT TTC AAA TCA ATG	1008
Leu Ala Gln Cys Gly Asp Lys Cys Ser Tyr Gly Thr Phe Lys Ser Met	
320 325 330 335	
CTA CAA AAA TAT AAC ATG GAG AAG GAA GCT CAT GAT AAA TTA TGT AAA	1056
Leu Gln Lys Tyr Asn Met Glu Lys Glu Ala His Asp Lys Leu Cys Lys	
340 345 350	
ACG TCG TAAAAATTAA AAATAAAAAC TTTTCAATAT ATTTTCCGCT AAAATAAATA	1112
Thr Ser	
AATATGTTTG TATATTTAAA CTTATCAAAA TAATAGTAGT GTTTTAATAA AGATTTTAAA	1172
TAAATAATTG TAAAAA AAAA AAAA AAAA AAAA AAAA	1205

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```

Glu Leu Lys Phe Val Phe Ala Thr Ala Arg Gly Met Ser His Thr Pro
 1              5              10              15
Cys Asp Tyr Pro Gly Gly Pro Lys Ile Thr His Lys Ser Glu Asp Ser
      20              25              30
Ser Gln Leu Thr Pro Ala Gly Gln Glu Glu Ala Leu Lys Ile Gly Lys
      35              40              45
Leu Leu Ser Glu His Tyr Arg Thr Asn Leu Lys Val Asp Lys Trp Asp
      50              55              60
Ser Asn Lys Asn Tyr Trp Thr Leu Ala Ser Ala Thr Arg Arg Ser Gln
      65              70              75              80
Glu Gly Ala Leu Ile Ile Gly Ser Gly Leu Glu Glu Lys Glu Lys Ala
      85              90              95
Val Trp Thr Lys Glu Lys Gly Asp Lys Thr Ile Phe Ser Ser Phe Gly
      100             105             110
Glu Tyr Ala Lys Phe Tyr Ser Pro Lys Thr Cys Pro Asn Phe Ile Ala
      115             120             125
Gln Gln Lys Ile Ala Val Arg Asp Leu Leu Thr Lys Ser Ala Lys Asp
      130             135             140
Tyr Lys Asn Ser Leu Ala Lys Leu Lys Glu Ala Tyr Lys Ile Asp Ala
      145             150             155             160
Thr Thr Ser Pro Gln Asn Val Trp Leu Ala Tyr Glu Thr Leu Asn Leu
      165             170             175
Gln Ser Lys Gln Asn Asn Ala Pro Thr Trp Trp Asn Thr Val Asn Lys
      180             185             190
Asp Leu Lys Gln Phe Ser Glu Lys Tyr Leu Trp Thr Ala Leu Thr Ser
      195             200             205
Asn Asp Asn Leu Arg Lys Met Ser Gly Gly Arg Met Ile Asn Asp Ile
      210             215             220
Leu Asn Asp Ile Glu Asn Ile Lys Lys Gly Glu Gly Gln Pro Gly Ala
      225             230             235             240
Pro Gly Gly Lys Glu Asn Lys Leu Ser Val Leu Thr Val Pro Gln Ala
      245             250             255
Ile Leu Ala Ala Phe Val Ser Ala Phe Ala Pro Glu Gly Thr Lys Ile
      260             265             270
Glu Asn Lys Asp Leu Asp Pro Ser Thr Leu Tyr Pro Gly Gln Gly Ala
      275             280             285

```

Leu His Val Ile Glu Leu His Gln Asp Lys Ser Asp Trp Ser Ile Lys
 290 295 300
 Val Leu Tyr Arg Asn Asn Asp Gln Met Lys Leu Lys Pro Met Lys Leu
 305 310 315 320
 Ala Gln Cys Gly Asp Lys Cys Ser Tyr Gly Thr Phe Lys Ser Met Leu
 325 330 335
 Gln Lys Tyr Asn Met Glu Lys Glu Ala His Asp Lys Leu Cys Lys Thr
 340 345 350
 Ser

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1205 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TTTTTTTTTT TTTTTTTTTT TTACAATTAT TTATTTAAAA TCTTTATTAA AACACTACTA	60
TTATTTTGAT AAGTTTAAAT ATACAAACAT ATTTATTTAT TTTAGCGGAA AATATATTGA	120
AAAGTTTTTA TTTTAAATTT TTACGACGTT TTACATAATT TATCATGAGC TTCCTTCTCC	180
ATGTTATATT TTTGTAGCAT TGATTTGAAA GTACCATAAG AACACTTGTC ACCGCATTGT	240
GCAAGTTTCA TTGGTTTCAG CTTCAATTTGG TCATTGTTTC TATAGAGAAC TTTTATGCTC	300
CAATCGCTCT TATCTGGTG TAGTTCAATA ACGTGAAGTG CTCCTTGGCC AGGATATAAA	360
GTAGACGGAT CAAGGTCCTT ATTTTCAATT TTTGTACCTT CGGGAGCAAA TGCTGAAACA	420
AATGCTGCTA AGATAGCTTG AGGAACGGTC AGCACTGATA ATTTGTTTTT CTTTCCTCCT	480
GGAGCACCCG GTTGTCCTTC TCCTTTCTTT ATGTTTTTCGA TATCGTTCAA TATATCGTTA	540
ATCATACGAC CTCCTGACAT CTTTCTAAGA TTATCATTAG AAGTCAAGGC GGTCCATAAA	600
TATTTCTCAG AGAATTGTTT TAGATCTTTG TTTACAGTAT TCCACCATGT TGGAGCGTTA	660
TTTTGCTTGC TTTGTAAATT CAAAGTTTCA TATGCCAGCC AAACATTCTG AGGGCTTGTC	720
GTCGCATCTA TTTTATACGC TTCTTTTAAT TTTGCAAGTG AATTTTTATA ATCTTTTGCA	780
CTTTTTGTGA ACAAGTCTCT TACTGCTATT TTCTGTTGTG CTATGAAGTT TGGACAAGTT	840
TTTGGAATAT AAAATTTAGC ATATTCACCA AACGAAGAAA ATATGGTTTT ATCTCCTTTC	900
TCTTTTGTCC AAAGTGCCTT TTCCTTTTCT TCTAGACCAG AACCAATGAT AAGCGCTCCT	960
TCTTGAGATC TTCTCGTAGC ACTAGCTAAT GTCCAATAAT TTTTATTGA ATCCCATTG	1020

TCAACTTTTA AATTAGTTCT GTAATGTTTCG GATAATAATT TGCCAATTTT TAATGCCTCT 1080
TCTTGACCTG CCGGTGTCAA TTGGCTTGAA TCTTCAGACT TGTGTGTAAT TTTTGGACCG 1140
CCTGGATAAT CACAAGGTGT ATGTGACATA CCTCGTGCGAG TCGCAAACAC AAATTTCAAT 1200
TCTGC 1205

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GAA TTG AAA TTT GTG TTT GCG ACT GCA CGA GGT ATG TCA CAT ACA CCT 48
Glu Leu Lys Phe Val Phe Ala Thr Ala Arg Gly Met Ser His Thr Pro
1 5 10 15

TGT GAT TAT CCA GGC GGT CCA AAA ATT ACA CAC AAG TCT GAA GAT TCA 96
Cys Asp Tyr Pro Gly Gly Pro Lys Ile Thr His Lys Ser Glu Asp Ser
20 25 30

AGC CAA TTG ACA CCG GCA GGT CAA GAA GAG GCA TTA AAA ATT GGC AAA 144
Ser Gln Leu Thr Pro Ala Gly Gln Glu Glu Ala Leu Lys Ile Gly Lys
35 40 45

TTA TTA TCC GAA CAT TAC AGA ACT AAT TTA AAA GTT GAC AAA TGG GAT 192
Leu Leu Ser Glu His Tyr Arg Thr Asn Leu Lys Val Asp Lys Trp Asp
50 55 60

TCA AAT AAA AAT TAT TGG ACA TTA GCT AGT GCT ACG AGA AGA TCT CAA 240
Ser Asn Lys Asn Tyr Trp Thr Leu Ala Ser Ala Thr Arg Arg Ser Gln
65 70 75 80

GAA GGA GCG CTT ATC ATT GGT TCT GGT CTA GAA GAA AAG GAA AAG GCA 288
Glu Gly Ala Leu Ile Ile Gly Ser Gly Leu Glu Glu Lys Glu Lys Ala
85 90 95

GTT TGG ACA AAA GAG AAA GGA GAT AAA ACC ATA TTT TCT TCG TTT GGT 336
Val Trp Thr Lys Glu Lys Gly Asp Lys Thr Ile Phe Ser Ser Phe Gly
100 105 110

GAA TAT GCT AAA TTT TAT AGT CCA AAA ACT TGT CCA AAC TTC ATA GCA 384
Glu Tyr Ala Lys Phe Tyr Ser Pro Lys Thr Cys Pro Asn Phe Ile Ala
115 120 125

CAA CAG AAA ATA GCA GTA AGA GAC TTG TTA ACA AAA AGT GCA AAA GAT 432
Gln Gln Lys Ile Ala Val Arg Asp Leu Leu Thr Lys Ser Ala Lys Asp
130 135 140

TAT AAA AAT TCA CTT GCA AAA TTA AAA GAA GCG TAT AAA ATA GAT GCG Tyr Lys Asn Ser Leu Ala Lys Leu Lys Glu Ala Tyr Lys Ile Asp Ala 145 150 155 160	480
ACG ACA AGC CCT CAG AAT GTT TGG CTG GCA TAT GAA ACT TTG AAT TTA Thr Thr Ser Pro Gln Asn Val Trp Leu Ala Tyr Glu Thr Leu Asn Leu 165 170 175	528
CAA AGC AAG CAA AAT AAC GCT CCA ACA TGG TGG AAT ACT GTA AAC AAA Gln Ser Lys Gln Asn Asn Ala Pro Thr Trp Trp Asn Thr Val Asn Lys 180 185 190	576
GAT CTA AAA CAA TTC TCT GAG AAA TAT TTA TGG ACC GCC TTG ACT TCT Asp Leu Lys Gln Phe Ser Glu Lys Tyr Leu Trp Thr Ala Leu Thr Ser 195 200 205	624
AAT GAT AAT CTT AGA AAG ATG TCA GGA GGT CGT ATG ATT AAC GAT ATA Asn Asp Asn Leu Arg Lys Met Ser Gly Gly Arg Met Ile Asn Asp Ile 210 215 220	672
TTG AAC GAT ATC GAA AAC ATA AAG AAA GGA GAG GGA CAA CCG GGT GCT Leu Asn Asp Ile Glu Asn Ile Lys Lys Gly Glu Gly Gln Pro Gly Ala 225 230 235 240	720
CCA GGA GGA AAG GAA AAC AAA TTA TCA GTG CTG ACC GTT CCT CAA GCT Pro Gly Gly Lys Glu Asn Lys Leu Ser Val Leu Thr Val Pro Gln Ala 245 250 255	768
ATC TTA GCA GCA TTT GTT TCA GCA TTT GCT CCC GAA GGT ACA AAA ATT Ile Leu Ala Ala Phe Val Ser Ala Phe Ala Pro Glu Gly Thr Lys Ile 260 265 270	816
GAA AAT AAG GAC CTT GAT CCG TCT ACT TTA TAT CCT GGC CAA GGA GCA Glu Asn Lys Asp Leu Asp Pro Ser Thr Leu Tyr Pro Gly Gln Gly Ala 275 280 285	864
CTT CAC GTT ATT GAA CTA CAC CAA GAT AAG AGC GAT TGG AGC ATA AAA Leu His Val Ile Glu Leu His Gln Asp Lys Ser Asp Trp Ser Ile Lys 290 295 300	912
GTT CTC TAT AGA AAC AAT GAC CAA ATG AAG CTG AAA CCA ATG AAA CTT Val Leu Tyr Arg Asn Asn Asp Gln Met Lys Leu Lys Pro Met Lys Leu 305 310 315 320	960
GCA CAA TGC GGT GAC AAG TGT TCT TAT GGT ACT TTC AAA TCA ATG CTA Ala Gln Cys Gly Asp Lys Cys Ser Tyr Gly Thr Phe Lys Ser Met Leu 325 330 335	1008
CAA AAA TAT AAC ATG GAG AAG GAA GCT CAT GAT AAA TTA TGT AAA ACG Gln Lys Tyr Asn Met Glu Lys Glu Ala His Asp Lys Leu Cys Lys Thr 340 345 350	1056
TCG Ser	1059

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Glu Leu Lys Phe Val Phe Ala Thr Ala Arg Gly Met Ser His Thr Pro
1 5 10 15
Cys Asp Tyr Pro Gly Gly Pro Lys Ile Thr His Lys Ser Glu Asp Ser
20 25 30
Ser Gln Leu Thr Pro Ala Gly Gln Glu Glu Ala Leu Lys Ile Gly Lys
35 40 45
Leu Leu Ser Glu His Tyr Arg Thr Asn Leu Lys Val Asp Lys Trp Asp
50 55 60
Ser Asn Lys Asn Tyr Trp Thr Leu Ala Ser Ala Thr Arg Arg Ser Gln
65 70 75 80
Glu Gly Ala Leu Ile Ile Gly Ser Gly Leu Glu Glu Lys Glu Lys Ala
85 90 95
Val Trp Thr Lys Glu Lys Gly Asp Lys Thr Ile Phe Ser Ser Phe Gly
100 105 110
Glu Tyr Ala Lys Phe Tyr Ser Pro Lys Thr Cys Pro Asn Phe Ile Ala
115 120 125
Gln Gln Lys Ile Ala Val Arg Asp Leu Leu Thr Lys Ser Ala Lys Asp
130 135 140
Tyr Lys Asn Ser Leu Ala Lys Leu Lys Glu Ala Tyr Lys Ile Asp Ala
145 150 155 160
Thr Thr Ser Pro Gln Asn Val Trp Leu Ala Tyr Glu Thr Leu Asn Leu
165 170 175
Gln Ser Lys Gln Asn Asn Ala Pro Thr Trp Trp Asn Thr Val Asn Lys
180 185 190
Asp Leu Lys Gln Phe Ser Glu Lys Tyr Leu Trp Thr Ala Leu Thr Ser
195 200 205
Asn Asp Asn Leu Arg Lys Met Ser Gly Gly Arg Met Ile Asn Asp Ile
210 215 220
Leu Asn Asp Ile Glu Asn Ile Lys Lys Gly Glu Gly Gln Pro Gly Ala
225 230 235 240
Pro Gly Gly Lys Glu Asn Lys Leu Ser Val Leu Thr Val Pro Gln Ala
245 250 255
Ile Leu Ala Ala Phe Val Ser Ala Phe Ala Pro Glu Gly Thr Lys Ile
260 265 270
Glu Asn Lys Asp Leu Asp Pro Ser Thr Leu Tyr Pro Gly Gln Gly Ala
275 280 285

Leu His Val Ile Glu Leu His Gln Asp Lys Ser Asp Trp Ser Ile Lys
 290 295 300
 Val Leu Tyr Arg Asn Asn Asp Gln Met Lys Leu Lys Pro Met Lys Leu
 305 310 315 320
 Ala Gln Cys Gly Asp Lys Cys Ser Tyr Gly Thr Phe Lys Ser Met Leu
 325 330 335
 Gln Lys Tyr Asn Met Glu Lys Glu Ala His Asp Lys Leu Cys Lys Thr
 340 345 350
 Ser

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1059 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CGACGTTTTA CATAATTTAT CATGAGCTTC CTTCTCCATG TTATAATTTT GTAGCATTGA	60
TTTGAAAGTA CCATAAGAAC ACTTGTCAAC GCATTGTGCA AGTTTCATTG GTTTCAGCTT	120
CATTTGGTCA TTGTTTCTAT AGAGAACTTT TATGCTCCAA TCGCTCTTAT CTGGGTGTAG	180
TTCAATAACG TGAAGTGCTC CTTGGCCAGG ATATAAAGTA GACGGATCAA GGTCTTTATT	240
TTCAATTTTT GTACCTTCGG GAGCAAATGC TGAAACAAAT GCTGCTAAGA TAGCTTGAGG	300
AACGGTCAGC ACTGATAATT TGTTTTCTT TCCTCCTGGA GCACCCGGTT GTCCCTCTCC	360
TTTCTTTATG TTTTCGATAT CGTTCAATAT ATCGTTAATC ATACGACCTC CTGACATCTT	420
TCTAAGATTA TCATTAGAAG TCAAGGCGGT CCATAAATAT TTCTCAGAGA ATTGTTTTAG	480
ATCTTTGTTT ACAGTATTCC ACCATGTTGG AGCGTTATTT TGCTTGCTTT GTAAATTCAA	540
AGTTTCATAT GCCAGCCAAA CATTCTGAGG GCTTGTGCTC GCATCTATTT TATACGCTTC	600
TTTTAATTTT GCAAGTGAAT TTTTATAATC TTTTGCACTT TTTGTAAACA AGTCTCTTAC	660
TGCTATTTTC TGTTGTGCTA TGAAGTTTGG ACAAGTTTTT GGACTATAAA ATTTAGCATA	720
TTCACCAAAC GAAGAAAATA TGGTTTTATC TCCTTTCTCT TTTGTCCAAA CTGCCTTTTC	780
CTTTTCTTCT AGACCAGAAC CAATGATAAG CGCTCCTTCT TGAGATCTTC TCGTAGCACT	840
AGCTAATGTC CAATAATTTT TATTTGAATC CCATTTGTCA ACTTTTAAAT TAGTTCTGTA	900
ATGTTCCGAT AATAATTTGC CAATTTTAA TGCCTCTTCT TGACCTGCCG GTGTCAATTG	960
GCTTGAATCT TCAGACTTGT GTGTAATTTT TGGACCGCCT GGATAATCAC AAGGTGTATG	1020

TGACATACCT CGTGCACTCG CAAACACAAA TTTCAATTC

1059

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Xaa = any amino acid
 - (B) LOCATION: 1

- (ix) FEATURE:
 - (A) NAME/KEY: Xaa = any amino acid
 - (B) LOCATION: 24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Xaa	Glu	Leu	Lys	Phe	Val	Phe	Val	Met	Val	Lys	Gly	Pro	Asp	His	Glu
1			5					10					15		
Ala	Cys	Asn	Tyr	Ala	Gly	Gly	Xaa	Gln							
			20					25							

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 406 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ATG	GTT	AAA	GGT	CCA	GAT	CAC	GAA	GCT	TGT	AAC	TAT	GCA	GGA	GGT	CCT	48
Met	Val	Lys	Gly	Pro	Asp	His	Glu	Ala	Cys	Asn	Tyr	Ala	Gly	Gly	Pro	
1			5					10					15			
CAG	TTA	ACT	ACT	CTT	CAA	GAA	AAA	GAT	AGT	GTT	CTA	ACT	GAA	GAT	GGC	96
Gln	Leu	Thr	Thr	Leu	Gln	Glu	Lys	Asp	Ser	Val	Leu	Thr	Glu	Asp	Gly	
			20				25					30				
AAG	ACA	GAA	GCA	TAC	GAA	TTG	GGA	AAA	CTT	TTG	GAC	AAG	GTA	TAT	AAA	144
Lys	Thr	Glu	Ala	Tyr	Glu	Leu	Gly	Lys	Leu	Leu	Asp	Lys	Val	Tyr	Lys	
			35				40					45				
AAA	CAA	TTA	AAA	GTT	GAC	AAA	TGG	GAT	GCC	ACG	AAA	ACC	TAC	TGG	GCT	192
Lys	Gln	Leu	Lys	Val	Asp	Lys	Trp	Asp	Ala	Thr	Lys	Thr	Tyr	Trp	Ala	
			50				55					60				

GTG TCC ACA AAA GCT ATG CGT ACT AAA GAA GCA GCC TTA ATT GTA GGA 240
Val Ser Thr Lys Ala Met Arg Thr Lys Glu Ala Ala Leu Ile Val Gly
65 70 75 80

GCA GGA TTG GAA AAT AAT CCT GCA AAA GCT AAA GGT AAT TGG ACA CAA 288
Ala Gly Leu Glu Asn Asn Pro Ala Lys Ala Lys Gly Asn Trp Thr Gln
85 90 95

CAA CAG CTC GAT TCA ACA CAT TTT GAT GCG ATG CCT GGC TTT TCT AGA 336
Gln Gln Leu Asp Ser Thr His Phe Asp Ala Met Pro Gly Phe Ser Arg
100 105 110

TTT TGG AAT CCT CAA CAA TGT CCG GCA TAT TTC AGA GCG CTC TCG CTA 384
Phe Trp Asn Pro Gln Gln Cys Pro Ala Tyr Phe Arg Ala Leu Ser Leu
115 120 125

CAA AAT CAG AAA ATA AAG AAA T 406
Gln Asn Gln Lys Ile Lys Lys
130 135

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met Val Lys Gly Pro Asp His Glu Ala Cys Asn Tyr Ala Gly Gly Pro
1 5 10 15

Gln Leu Thr Thr Leu Gln Glu Lys Asp Ser Val Leu Thr Glu Asp Gly
20 25 30

Lys Thr Glu Ala Tyr Glu Leu Gly Lys Leu Leu Asp Lys Val Tyr Lys
35 40 45

Lys Gln Leu Lys Val Asp Lys Trp Asp Ala Thr Lys Thr Tyr Trp Ala
50 55 60

Val Ser Thr Lys Ala Met Arg Thr Lys Glu Ala Ala Leu Ile Val Gly
65 70 75 80

Ala Gly Leu Glu Asn Asn Pro Ala Lys Ala Lys Gly Asn Trp Thr Gln
85 90 95

Gln Gln Leu Asp Ser Thr His Phe Asp Ala Met Pro Gly Phe Ser Arg
100 105 110

Phe Trp Asn Pro Gln Gln Cys Pro Ala Tyr Phe Arg Ala Leu Ser Leu
115 120 125

Gln Asn Gln Lys Ile Lys Lys
130 135

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 406 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```

ATTCTTTTAT TTTCTGATTT TGTAGCGAGA GCGCTCTGAA ATATGCCGGA CATTGTTGAG      60
GATTCCAAAA TCTAGAAAAG CCAGGCATCG CATCAAAATG TGTTGAATCG AGCTGTTGTT      120
GTGTCCAATT ACCTTTAGCT TTTGCAGGAT TATTTTCCAA TCCTGCTCCT ACAATTAAGG      180
CTGCTTCTTT AGTACGCATA GCTTTTGTGG ACACAGCCCA GTAGGTTTTC GTGGCATCCC      240
ATTTGTCAAC TTTTAATTGT TTTTATATA CCTTGTCCAA AAGTTTCCC AATTCGTATG      300
CTTCTGTCTT GCCATCTTCA GTTAGAACAC TATCTTTTTC TTGAAGAGTA GTTAACTGAG      360
GACCTCCTGC ATAGTTACAA GCTTCGTGAT CTGGACCTTT AACCAT                      406
  
```

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 420 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

GAA GTT ATG GAT AAA TTG CGA AAA CAG GCA CCT CCT AAA ACT GAT GGC      48
Glu Val Met Asp Lys Leu Arg Lys Gln Ala Pro Pro Lys Thr Asp Gly
  1             5             10            15

AAT CCT CCA AAA ACA ACC ATA ATG AGT ACA CTT CAA AAG CAA CAA ATA      96
Asn Pro Pro Lys Thr Thr Ile Met Ser Thr Leu Gln Lys Gln Gln Ile
          20             25            30

AGT TGC ACA GAA GTG AAA GCG GTT AAC TTA GAA AGT CAT GTT TGT GCT      144
Ser Cys Thr Glu Val Lys Ala Val Asn Leu Glu Ser His Val Cys Ala
          35             40            45

TAT GAT TGT AGT CAA CCT GAA ACT GCA GGA ATT ACA TGC AAA GGA AAT      192
Tyr Asp Cys Ser Gln Pro Glu Thr Ala Gly Ile Thr Cys Lys Gly Asn
          50             55            60

AAG TGT GAT TGT CCT AAA AAA CGC TAAAAATTTA TTCAAAACAT TTACATTTTT      246
Lys Cys Asp Cys Pro Lys Lys Arg
          65             70
  
```

TATTAATATT CAACTATCAA AAATTCTGTG TTGATTGTTA TTATATTTAT CATAGTTACT 306
 AGAAATAAAA TTTTATAACA TTGTTAATTC GAAATTGAAT ACACATAATA TTATAATTAG 366
 TGAGGTTAAA AGAAATAAAC CGAATATCCA AATCAAAAAA AAAAAAAAAA AAAA 420

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Glu Val Met Asp Lys Leu Arg Lys Gln Ala Pro Pro Lys Thr Asp Gly
 1 5 10 15
 Asn Pro Pro Lys Thr Thr Ile Met Ser Thr Leu Gln Lys Gln Ile
 20 25 30
 Ser Cys Thr Glu Val Lys Ala Val Asn Leu Glu Ser His Val Cys Ala
 35 40 45
 Tyr Asp Cys Ser Gln Pro Glu Thr Ala Gly Ile Thr Cys Lys Gly Asn
 50 55 60
 Lys Cys Asp Cys Pro Lys Lys Arg
 65 70

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 420 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TTTTTTTTTT TTTTTTTTTT GATTGATA TTCGGTTTAT TTCTTTTAAC CTCACTAATT 60
 ATAATATTAT GTGTATTCAA TTTCGAATTA ACAATGTTAT AAAATTTTAT TTCTAGTAAC 120
 TATGATAAAT ATAATAACAA TCAACACAGA ATTTTGTGATA GTTGAATATT AATAAAAAAT 180
 GTAAATGTTT TGAATAAATT TTTAGCGTTT TTTAGGACAA TCACACTTAT TTCCTTTGCA 240
 TGTAATTCCT GCAGTTTCAG GTTGACTACA ATCATAAGCA CAAACATGAC TTTCTAAGTT 300
 AACCGCTTTC ACTTCTGTGC AACTATTTTG TTGCTTTTGA AGTGTACTCA TTATGGTTGT 360
 TTTTGGAGGA TTGCCATCAG TTTTAGGAGG TGCCTGTTTT CGCAATTAT CCATAACTTC 420

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```

Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser
1              5              10              15

Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe
              20              25              30

Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys Ser Gln Cys
              35              40              45

Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr Arg Pro Asn
50              55              60

Gln Lys His Cys Tyr Cys Glu
65              70

```

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```

Asn Asp Lys Leu Gln Phe Val Phe Val Met Ala Arg Gly Pro Asp His
1              5              10              15

Glu Ala Cys Asn Tyr Pro Gly Gly Pro
              20              25

```

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..26
 - (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AGTGGATCCG TCAAAAATGG TCACTG

26

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CCGGAATTCT GTTATTCGCA ATAACAGT

28

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CCGCGGATCC GCATATGGAA GACATCTGGA AAGTTAATAA AAAATGTACA TCAG

54

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CCGGAATTCT TATTTATTTT TTGGTCGACA ATAACAAAAG TTTCC

45

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

AAATTTGTWT TTGTWATGGT WAAAGGWCCW GATCATGAAG C

41

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..37
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CATGAACCWG GWAATACWCG WAARATHAS

29

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTAAAACGAC GGCCAGT

17

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..31
 - (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GAAGTWATGG AYAAATTRAG RCARGC

26

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Tyr	Phe	Asn	Lys	Leu	Val	Gln	Ser	Trp	Thr	Glu	Pro	Met	Val	Phe	Lys
1				5					10					15	

Tyr Pro Tyr

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..24
 - (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTAATACGAC TCACTATATA GGGC

24